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QY 1 GCACTAAAAACACATCATGAGAGCTCCGAACTCCACCTTGAGAGGGCTTCATCTT 60
Db 1 GCACTAAAAACACATCATGAGAGCTCCGAACTCCACCTTGAGAGGGCTTCATCTT 60
QY 61 GGTGGGAGATTCGATGACAGTGGGCTCTCTGAACTGCTCTATGATTAACAATCTT 120
Db 61 GGTGGGAGATTCGATGACAGTGGGCTCTCTGAACTGCTCTATGATTAACAATCTT 120
QY 121 ATTCATGTTGGGACCTGACCAAGCAATGGTCTGCTGCTCCGCAATCAACATAGAGCCG 180
Db 121 ATTCATGTTGGGACCTGACCAAGCAATGGTCTGCTGCTCCGCAATCAACATAGAGCCG 180
QY 181 GCTCCACATGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 181 GCTCCACATGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 241 ATCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db 241 ATCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 301 TGGAGGCTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Db 301 TGGAGGCTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 361 ACTGAGCTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 361 ACTGAGCTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 421 CCTCATGAGCCCAAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 421 CCTCATGAGCCCAAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 481 GATTGCTATGAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
Db 481 GATTGCTATGAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
QY 541 CAGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db 541 CAGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 601 GTATGAGCTTATATATATATATATATATATATATATATATATATATATATATATAT 660
Db 601 GTATGAGCTTATATATATATATATATATATATATATATATATATATATATATATAT 660
QY 661 TGTGGCTCTTACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Db 661 TGTGGCTCTTACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
QY 721 GAAAGAAAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 721 GAAAGAAAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
QY 781 TGGCAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
Db 781 TGGCAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY 841 CTCTGTTTTCACAAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
Db 841 CTCTGTTTTCACAAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
QY 901 TAAAGAGGTCATGAGGCTTGAAGAGGCTTGAAGAGGCTTGAAGAGGCTTGAAGAGGCT 960
Db 901 TAAAGAGGTCATGAGGCTTGAAGAGGCTTGAAGAGGCTTGAAGAGGCTTGAAGAGGCT 960
QY 961 CAGGCTCTAGGGAAGGA 977
Db 961 CAGGCTCTAGGGAAGGA 977

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RESULT 2
 US-09-777-789-8
 ; Sequence 8, Application US/09777789
 ; Publication No. US20030087815A1

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; GENERAL INFORMATION:
; APPLICANT: Padigaru et al.
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-654
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/180,646
; PRIOR FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 8
; LENGTH: 1050
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-777-789-8

Query Match      85.5%; Score 835; DB 10; Length 1050;
Best Local Similarity 91.2%; Pred. No. 1,2e-268;
Matches 886; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 7 AAAAAACACATCATGAGAGCTCCGAACTCCACCTTGAGAGGGCTTCATCTTGTGGG 66
Db 59 AAGAAACACAGATGAGAGCTCCGAACTCCACCTTGAGAGGGCTTCATCTTGTGGG 118
QY 67 GATTCTGATGACAGTGGGCTCTCTGAACTGCTCTATGCTTACATTTACATCTTATCAT 126
Db 119 GATTCTGATGACAGTGGGCTCTCTGAACTGCTCTGCTGCTTACATTTACATCTTATCAT 178
QY 127 GTTGGACATGACAGGAATGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 186
Db 179 GTTGGCCCTGATGACAGGAATGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 238
QY 187 CATGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 246
Db 239 CATGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 298
QY 247 TGTGATCTCCAAAGGCTTGGCGGACTTTCTGCGCAGAGAAACAATATCTCTTTGGAGG 306
Db 299 TGTGATCTCCAAAGGCTTGGCGGACTTTCTGCGCAGAGAAACAATATCTCTTTGGAGG 358
QY 307 CTGTGACATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 366
Db 359 CTGTGACATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 418
QY 367 CTTCATGAGCTTATGACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 426
Db 419 CTTCATGAGCTTATGACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 478
QY 427 GAGCCAAAGAGTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 486
Db 479 GAGCCAAAGAGTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 538
QY 487 TATAGGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 546
Db 539 CTAATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 598
QY 547 TCTGCTGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 606
Db 599 TCTTCTGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 658
QY 607 GCTTATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 666
Db 659 GCTTATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 718
QY 667 CTCTTACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 726
Db 719 CTCTTATACAAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 778
QY 727 AGCCCTTGTGACCTGCTCTTCCACCTGATGATGATGATGATGATGATGATGATGATGATGAT 786
Db 779 AGCCCTTGTGACCTGCTCTTCCACCTGATGATGATGATGATGATGATGATGATGATGATGAT 838
QY 787 ATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 846

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Db 839 ATTCAATGATGCTCTGCGCAGTTTCCTTCACAGACACGAAAGCAACATCATCTCTGT 898
QY 847 TTTCTACACAATTTGTCACTCCAGCCCTGAAATCCACTCATCTACAGCCTGAGAAATAAGA 906
Db 899 TTTCTACACAATTTGTCACTCCAGCCCTGAAATCCACTCATCTACAGCCTGAGAAATAAGA 958
QY 907 GGTCAATGCGGGCCTTGAAGAGGGTCTCTGGGAAAAATACATACCTGTCACATTCACGCT 966
Db 959 GGTCAATGCGGGCCTTGAAGAGGGTCTCTGGGAAAAATACATACCTGTCACATTCACGCT 1018
QY 967 CTAGGGAAGGA 977
Db 1019 CTAGGGAAGGA 1029
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RESULT 3
US-10-017-161-309
; Sequence 309, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUMA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YURAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; PRIOR FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 309
; LENGTH: 1351
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: source
; LOCATION: (1)..(1351)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(1151)
US-10-017-161-309
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Query Match 85.5%; Score 835; DB 15; Length 1351;
Best local Similarity 91.2%; Pred. No. 1,4e-268;
Matches 886; Conservative 0; Mismatches 85; Indels 0; Gaps 0;
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QY 7 AAAAAAAAAACATCATGAGCTCCGGAACCTCCACCTTGGGAAGCGGCTTCATCTTGTGGG 66
Db 188 AAGAAACACACAGATGAGCTCTGGAATCTCACTTGGGAAGTGGCTTCAATTTGGTGGG 247
QY 67 GATTCTGAATGACAGTGGGTCTCTGTAAGTCTGTATGCTACATTTACATCCATATCAT 126
Db 248 GATTCTGAATGACAGTGGGTCTCTGTAAGTCTGTATGCTACATTTACATCCATATCAT 307
QY 127 GTTGGACATGACGACGAATGATGCTGCTCTGGGACCATCACTAGAGCCGCGCTCCA 186
Db 308 GTTGGACATGACGACGAATGATGCTGCTCTGGGACCATCACTAGAGCCGCGCTCCA 367
QY 187 CATGCCCATGTAATCTCTGCTTGGGACGCTCTCTCATGGAAGCTCTCTGTTCAATCTGT 246
Db 368 CATGCCCATGTAATCTCTGCTTGGGACGCTCTCTCATGGAAGCTCTCTGTTCAATCTGT 427
QY 247 TGTCACTCCCAAGGCTTGGCGGACTTTCTGCGGAGAGAAAAACATATCTCTTGGAGG 306
Db 428 TGTCACTCCCAAGGCTTGGCGGACTTTCTGCGGAGAGAAAAACATATCTCTTGGAGG 487
QY 307 CTGTGACCTTCAGATGTTCTCGGACATGACAAATGGGTAGGCGCTGAGGACCTCTACTGGC 366
Db 488 CTGTGACCTTCAGATGTTCTCGGACATGACAAATGGGTAGGCGCTCTACTGGC 547
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QY 367 CTTCATGGCCTATGACAGGTATGTGGCCATTTGTATCTCTGTAATATACATGACCTCAT 426
Db 548 CTTCATGGCCTATGACAGGTATGTGGCCATTTGTATCTCTGTAATATACATGACCTCAT 607
QY 427 GAGCCCAAGATGTGCTGATCATGCTGGGCAATCTCTGGATCTCTGATCTCTGATTTGC 486
Db 608 GAGCTCAAGAGCTGTGCTGATCATGCTGGGCAATCTCTGGATCTCTGATCTCTGATTTGC 667
QY 487 TATAGACATACCATGATTAACATGACCTCTCTGATGATGCTCTGATGATGATGATGAT 546
Db 668 CTTATATATATACCGTGTATATGATGATGATGATGATGATGATGATGATGATGATGAT 727
QY 547 TCTGCTCTGTGATATCCACCTCTGATGATGATGATGATGATGATGATGATGATGATGAT 606
Db 728 TCTTCTGTGATATCCACCTCTGATGATGATGATGATGATGATGATGATGATGATGAT 787
QY 607 GCTTATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 666
Db 788 GCTTATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 847
QY 667 CTCTTACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 726
Db 848 CTCTTATACACAAATTTCTACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 907
QY 727 AGCCCTTGTACCTGCTCTTCCACCTGATGATGATGATGATGATGATGATGATGATGATGAT 786
Db 908 AGCCCTTGTACCTGCTCTTCCACCTGATGATGATGATGATGATGATGATGATGATGATGAT 967
QY 787 ATTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 846
Db 968 ATTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1027
QY 847 TTTCTACACAATTTGTCACTCCAGCCCTGAAATCCACTCATCTACAGCCTGAGAAATAAGA 906
Db 1028 TTTCTACACAATTTGTCACTCCAGCCCTGAAATCCACTCATCTACAGCCTGAGAAATAAGA 1087
QY 907 GGTCAATGCGGGCCTTGAAGAGGGTCTCTGGGAAAAATACATACCTGTCACATTCACGCT 966
Db 1088 GGTCAATGCGGGCCTTGAAGAGGGTCTCTGGGAAAAATACATACCTGTCACATTCACGCT 1147
QY 967 CTAGGGAAGGA 977
Db 1148 CTAGGGAAGGA 1158
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RESULT 4
US-10-292-798-275
; Sequence 275, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUMA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YURAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 275
; LENGTH: 1351
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: source
; LOCATION: (1)..(1351)
; FEATURE:
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? PRIOR APPLICATION NUMBER: 60/323,755
? PRIOR FILING DATE: 2001-09-20
? NUMBER OF SEQ ID NOS: 26
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 11
? LENGTH: 1008
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (27)..(998)
?
? US-09-974-149-11

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85.4%; Score 834; DB 10; Length 1008;

QY	6	AAAAAACATCATGAGCTCCGGAAATCCACCTTGGAGACGGCTCACTTGGTGGG	67
Dp	39	AACATACCAAGCATGGAGCTCTGGAACCTCAACCTTGGGAATGGCTCATTTTGGTGGG	98
QY	68	ATTCTGAATGACAGTGGGCTCTCTGAACTGCTCTATGTGTAATTTACATTCATATAC	127
Dp	99	ATTCTGAATGACAGTGGGCTCTCTGAACTGCTCTGTTGCTAACATTTACATTCATATAC	158
QY	128	TTGGCACTACACAGCAATGGTCTGGTCCCTGGCAATCACATATAGAAAGCCGGCTCAC	187
Dp	159	TTGGCCCTATACAGCAATGGCTTACTGCTCTGGCTATACATATAGAAAGCCGGCTCAC	218
QY	188	ATGCCCATGTACTCTCTGGTGGGAGCTCTCTCATAGACCTCTGTTCAATCTGTT	247
Dp	219	ATGCCCATGTACTCTCTGGTGGGAGCTCTCTCATAGACCTCTGTTCAATCTGTT	278
QY	248	GTTACTCTCCAAAGCCTTGGCGGACTTTCTGGCGAGAGAAAACTATCTCTTTGGAGGC	307
Dp	279	GTTACTCTCCAAAGCCTTGGCGGACTTTCTGGCGAGAGAAAACACATCTCTTTGGAGGC	338
QY	308	TGTGCACCTTCAGATGTTCTCTGGCACTGCACAAATGGGTTACGGCTGAGAGACTCTTAC	367
Dp	339	TGTGCCCTTCAAGTGTCTCTGGCACTGCACAAATGGGTTGCTGAGAGACTCTTAC	398
QY	368	TTTCATGGCCTATACACAGTATGTGGCAATTTGTCACTCTGAAATACATGACCCCTCATG	427
Dp	399	TTTCATGGCCTATACACAGTATGTGGCAATTTGTCACTCTGAAATACATGACCCCTCATG	458
QY	428	AGCCCAAGAGTCTCTGCGATTCATGTTGGCGACATCTCTGGAATCCTGATTTGCT	487
Dp	459	AGCTCAAGAGCCCTGCGGCTCATGTTGGCGAGTCTCTGGAATCCTGGAATCCTGGAATTTG	518
QY	488	ATAGGACATACATGACATGACATGACACCTCCCTTCTGTGTGCTGGGAAATCAGGCAT	547
Dp	519	CTATATATATACCGTGTATACATGACATATCCCTCTCTGAGGGCCAGAGATATAGGCAT	578
QY	548	CTGCTCTGAGAGTCCACCTTGTCTGAAGTTGGCCTGTGCTGATTACTCCAGTATGAG	607
Dp	579	CTTCTCTGAGAGTCCACACTTGTCTGAAGTTGGCCTGTGCTGATTACTCCAGTATGAG	638
QY	608	CTTATATATACGTTGACAGTGTGACTTCCCTCTGCTGCCATTTCTGCGCATGTGAGCC	667
Dp	639	CTATGATATATGTGATGGGTGTGACCTTCTCGATTCCTCTCTGTGCTATATCTGCC	698
QY	668	TTCCTACACTAGTCCATTTCACTGTGCTCTGATGCCATCAAAATGAGGGAGAGAGAAA	727
Dp	699	TTCCTATATACAAATTTCACTGTGCTCTGATGCCATCAAAATGAGGGAGAGAGAAA	758
QY	728	GCCCTTGTCACTGCTCTTCCACTGATTTGTGTGGGATGTTCTATGAGCTGCCACA	787
Dp	759	GCCCTTGTCACTGCTCTTCCACTGATTTGTGTGGGATGTTCTATGAGCTGCCACA	818
QY	788	TTTCATGTATGTCTTGGCCAGTCTCTTCCACAGCCCAAAAGAGCAATCATCTCTGTT	847
Dp	819	TTTCATGTATGTCTTGGCCAGTCTCTTCCACAGCCCAAAAGAGCAATCATCTCTGTT	878

QY	848	TTCTACACAATGTGAC	TCGACG	CCCTGAT	CCATCAT	CTACAGC	CTGAGAA	TTAAGAG	907
Db	879	TTCTACACAATTGTCA	CTCCAGC	CCCTGAT	CCATCAT	CTACAGC	CTGAGAA	TTAAGAG	938
QY	908	GTCATCGGAGCCTTGAG	GAGG	GGTCTCTGG	AAAAAT	CATAC	TGCTGG	ACATTC	967
Db	939	GTATCGGAGCCTTGAG	GAGG	GGTCTCTGG	AAAAAT	CATAC	TGCTGG	ACATTC	998
QY	968	TAGGAAAGA	977						
Db	999	TAGGAAAGA	1008						

RESULT 8
US-09-97

```

: Sequence 13 Application US/09974591
: Publication No. US20030059830A1
:
: GENERAL INFORMATION:
: APPLICANT: Alsobrook II, John P
: APPLICANT: Burgess, Catherine E
: APPLICANT: Grose, William M
: APPLICANT: Lepley, Denise M
: APPLICANT: Padigaru, Muralidhara
: APPLICANT: Spytek, Kimberly A
: TITLE OF INVENTION: No. US20030059830A1e1 Single Nucleotide Polymorphisms for Olfactor
: TITLE OF INVENTION: Receptor-like Polypeptides and Nucleic Acids Encoding
: TITLE OF INVENTION: The Same
: FILE REFERENCE: 15966-654 CIP
: CURRENT APPLICATION NUMBER: US/09/974,591
: CURRENT FILING DATE: 2001-10-09
: PRIOR APPLICATION NUMBER: 60/245,292
: PRIOR FILING DATE: 2000-11-02
: NUMBER OF SEQ ID NOS: 26
: SOFTWARE: PatentIn Ver. 2.1
:
: SEQ ID NO 13
:
: LENGTH: 1008
:
: TYPE: DNA
:
: ORGANISM: Homo sapiens
:
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (27)..(998)
:
: US-09-974-591-13

```

Query Match	85.2%;	Score 832.4;	DB 10;	Length 1008;
Best Local Similarity	91.1%;	Pred. No. 8.8e-268;		
Matches 884;	Conservative	0;	Mismatches 86;	Indels 0;
				Gaps 0;

QY	8	AAAAAACACATCATGGAGCTCCGGAACTCAACTTGGGAAAGCGGTTACTTGTGTGGG	67
Db	39	AACACACACAGATGAGGCTCTGAACTTCACTTGGGAAAGTGCGTTCAATTTGGTGGG	98
QY	68	ATTCTGAATACAGTGGGTCTCTGAACTCTATAGTCATATTACATCTTAAATG	127
Db	99	ATTCTGAATACAGTGGGTCTCTGAACTCTATAGTCATATTACATCTTAAATG	156
QY	128	TTGGCACTGACAGGCAATGTCTGCTGCTCCCTGGCAATCAACATAGAAAGCCCGCTCAC	187
Db	159	TTGGCCCTGTATGACAAATGACCCTACTGCTCTGTGCTATACATAGAAAGCCCGCTCAC	218
QY	188	ATGCCATGACCTCTGCTTGGGACGCTCTCTCATAGAACCTCTGTTCACATCTGT	247
Db	219	ATGCCATGACCTCTGCTTGGGACGCTCTCTCATAGAACCTCTGTTCACATCTGT	278
QY	248	GTCACCTCCCAAGGCTTTGGCGACCTTTCTGGCGAAGAAAAACATATCTCTTTGGAGGC	307
Db	279	GTCACCTCCCAAGGCTTTGGCGACCTTTCTGGCGAAGAAAAACATATCTCTTTGGAGGC	338
QY	308	TGTGCACTTACAGATGTTCTCGGACCTGACAATAGGGTAGCGTAGAGACCTCTACTGGCC	367
Db	339	TGTGCTCTTACAGATGTTCTCGGACCTGACAATAGGGTAGCGTAGAGACCTCTACTGGCC	398
QY	368	TTCAATGGCCTATGACAGATATGTGGCAATTTGTCAATCTCTGAAATACATGACCTCAATG	427

Db 399 TTCAATGCGCTATGACAGGATATGAGGCAATTGTGATCCTCTGACATACATGACCTCATG 458
Qy 428 AGCCCAAGATGCTGCTGATCATATGAGGCAATCTGGAATCTGGCAATCCCTGATTTGCT 487
Db 459 AGCTCAAGAGCTGCTGCTGATCATATGAGGCAATCTGGAATCTGGCAATCCCTGATTTGCT 518
Qy 488 ATAGACATACATGATATGACATATGACCTCTCTGATGATGCTGAGGAATCAAGAT 547
Db 519 CTAATATATACCGGTATATACATGACATATCTCTGACAGGCGCCAGAGATCAAGGAT 578
Qy 548 CTGCTCTGATGATCCCAAGCTTGGCTGAAAGTTGGCTGCTGATGATCTGACAGGATGAG 607
Db 579 CTCTCTGATGATGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 638
Qy 608 CTATATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 667
Db 639 CTATATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 698
Qy 668 TCCATACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 727
Db 699 TCCATATACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 758
Qy 728 GCGCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 787
Db 759 GCGCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 818
Qy 788 TTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 847
Db 819 TTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 878
Qy 848 TTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 907
Db 879 TTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 938
Qy 908 GTCAATGCGGCTTGAAGAGGAGGCTGAGGAATATACATGATGATGATGATGATGATGATG 967
Db 939 GTCAATGCGGCTTGAAGAGGAGGCTGAGGAATATACATGATGATGATGATGATGATGATG 998
Qy 968 TAGGGAAGA 977
Db 999 TAGGGAAGA 1008

RESULT 9
US-09-974-149-13
; Sequence 13, Application US/09974149
; Publication No. US20030175705A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook II, John P
; APPLICANT: Burgess, Catherine B
; APPLICANT: Groese, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Bader, Joel S
; APPLICANT: Bader, Aruna
; TITLE OF INVENTION: Methods of Use for No. US20030175705A1 Single Nucleotide
; TITLE OF INVENTION: Polymorphisms of Olfactory Receptor-like Polypeptides
; FILE REFERENCE: 15966-654UB
; CURRENT APPLICATION NUMBER: US/09/974,149
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/323,755
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (27)..(998)

US-09-974-149-13
Query Match 85.2%; Score 832.4; DB 10; Length 1008;
Best Local Similarity 91.1%; Pred. No. 8,88-268;
Matches 884; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

Qy 8 AAAAAACATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 67
Db 39 AACTATACACAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 98
Qy 68 ATTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 127
Db 99 ATTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 158
Qy 128 TTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 187
Db 159 TTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 218
Qy 188 ATGCCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 247
Db 219 ATGCCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 278
Qy 248 GTCACTCCCAAGGCTTGGAGGAGCTTCTGAGGAGAGAAACATATCTCTTGGAGGAGC 307
Db 279 GTCACTCCCAAGGCTTGGAGGAGCTTCTGAGGAGAGAAACATATCTCTTGGAGGAGC 338
Qy 308 TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 367
Db 339 TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 398
Qy 368 TTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 427
Db 399 TTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 458
Qy 428 AGCCCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 487
Db 459 AGCTCAAGAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 518
Qy 488 ATAGACATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 547
Db 519 CTAATATATACCGGTATATACATGATGATGATGATGATGATGATGATGATGATGATGATG 578
Qy 548 CTGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 607
Db 579 CTGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 638
Qy 608 CTATATATATACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 667
Db 639 CTATATATATACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 698
Qy 668 TCCATACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 727
Db 699 TCCATATACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 758
Qy 728 GCGCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 787
Db 759 GCGCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 818
Qy 788 TTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 847
Db 819 TTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 878
Qy 848 TTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 907
Db 879 TTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 938
Qy 908 GTCAATGCGGCTTGAAGAGGAGGCTGAGGAATATACATGATGATGATGATGATGATGATG 967
Db 939 GTCAATGCGGCTTGAAGAGGAGGCTGAGGAATATACATGATGATGATGATGATGATGATG 998
Qy 968 TAGGGAAGA 977
Db 999 TAGGGAAGA 1008

RESULT 13
 US-10-343-650A-513
 ; Sequence 513, Application US/10343650A
 ; Publication No. US20040067499A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HAGA, TATSUYA
 ; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
 ; FILE REFERENCE: 31671-186347
 ; CURRENT APPLICATION NUMBER: US/10/343,650A
 ; CURRENT FILING DATE: 2003-07-21
 ; PRIOR APPLICATION NUMBER: JP 2000/237818
 ; PRIOR FILING DATE: 2000-08-04
 ; PRIOR APPLICATION NUMBER: JP 2001/34434
 ; PRIOR FILING DATE: 2001-02-13
 ; NUMBER OF SEQ ID NOS: 694
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 513
 ; LENGTH: 951
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(951)
 US-10-343-650A-513

Query Match 83.9%; Score 819.8; DB 13; Length 951;
 Best Local Similarity 91.4%; Pred. No. 1.4e-263;
 Matches 869; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

20 ATGAGAGCTCCGGAAGCTCAGCTTGGAGAGCGGCTTCACTTGGTGGGAGTTCTGAATGAC 79
 1 ATGAGAGCTCCGGAAGCTCAGCTTGGAGAGCGGCTTCACTTGGTGGGAGTTCTGAATGAC 60
 80 AGTGGGTCTCCGGAAGCTCAGCTTGGAGAGCGGCTTCACTTGGTGGGAGTTCTGAATGAC 139
 61 AGTGGGTCTCCGGAAGCTCAGCTTGGAGAGCGGCTTCACTTGGTGGGAGTTCTGAATGAC 120
 140 AGCAATGCTCGTGGAGAGCTCAGCTTGGAGAGCGGCTTCACTTGGTGGGAGTTCTGAATGAC 199
 121 AGCAATGCTCGTGGAGAGCTCAGCTTGGAGAGCGGCTTCACTTGGTGGGAGTTCTGAATGAC 180
 200 CTCCTGGTGGAGAGCTCAGCTTGGAGAGCGGCTTCACTTGGTGGGAGTTCTGAATGAC 259
 181 CTCCTGGTGGAGAGCTCAGCTTGGAGAGCGGCTTCACTTGGTGGGAGTTCTGAATGAC 240
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 380 GACAGGATGAGAGCTCAGCTTGGAGAGCGGCTTCACTTGGTGGGAGTTCTGAATGAC 439
 361 GACAGGATGAGAGCTCAGCTTGGAGAGCGGCTTCACTTGGTGGGAGTTCTGAATGAC 420
 440 TGTGGATGAGAGCTCAGCTTGGAGAGCGGCTTCACTTGGTGGGAGTTCTGAATGAC 499
 421 TGTGGATGAGAGCTCAGCTTGGAGAGCGGCTTCACTTGGTGGGAGTTCTGAATGAC 480
 500 ATGTTCCGGAAGCTCAGCTTGGAGAGCGGCTTCACTTGGTGGGAGTTCTGAATGAC 559
 481 ATGTTCCGGAAGCTCAGCTTGGAGAGCGGCTTCACTTGGTGGGAGTTCTGAATGAC 540
 560 ATGTTCCGGAAGCTCAGCTTGGAGAGCGGCTTCACTTGGTGGGAGTTCTGAATGAC 619
 541 ATGTTCCGGAAGCTCAGCTTGGAGAGCGGCTTCACTTGGTGGGAGTTCTGAATGAC 600
 620 GTGAGAGGTTGAGAGCTCAGCTTGGAGAGCGGCTTCACTTGGTGGGAGTTCTGAATGAC 679
 601 GTGAGAGGTTGAGAGCTCAGCTTGGAGAGCGGCTTCACTTGGTGGGAGTTCTGAATGAC 660

★

Query 680 GTTCTATTCAGTGTGCTTGGATGAGAGCGGCTTCACTTGGTGGGAGTTCTGAATGAC 739
 661 ATGTTCCGGAAGCTCAGCTTGGAGAGCGGCTTCACTTGGTGGGAGTTCTGAATGAC 720
 740 TGTGGATGAGAGCTCAGCTTGGAGAGCGGCTTCACTTGGTGGGAGTTCTGAATGAC 799
 721 TGTGGATGAGAGCTCAGCTTGGAGAGCGGCTTCACTTGGTGGGAGTTCTGAATGAC 780
 800 TGTGGATGAGAGCTCAGCTTGGAGAGCGGCTTCACTTGGTGGGAGTTCTGAATGAC 859
 781 TGTGGATGAGAGCTCAGCTTGGAGAGCGGCTTCACTTGGTGGGAGTTCTGAATGAC 840
 860 GTGAGAGGTTGAGAGCTCAGCTTGGAGAGCGGCTTCACTTGGTGGGAGTTCTGAATGAC 919
 841 GTGAGAGGTTGAGAGCTCAGCTTGGAGAGCGGCTTCACTTGGTGGGAGTTCTGAATGAC 900
 920 TGTGGAGAGGTTGAGAGCTCAGCTTGGAGAGCGGCTTCACTTGGTGGGAGTTCTGAATGAC 970
 901 TGTGGAGAGGTTGAGAGCTCAGCTTGGAGAGCGGCTTCACTTGGTGGGAGTTCTGAATGAC 951

★

RESULT 14
 US-10-220-382-39
 ; Sequence 39, Application US/10220382
 ; Publication No. US2003011911A1
 ; GENERAL INFORMATION:
 ; APPLICANT: INCYTE GENOMICS, INC.
 ; APPLICANT: LAL, Preeti
 ; APPLICANT: TANG, Y. Tom
 ; APPLICANT: PATTERSON, Chandra
 ; APPLICANT: YAO, Monique G.
 ; APPLICANT: SHIH, Leo L.
 ; APPLICANT: TRIBOULEY, Catherine
 ; APPLICANT: LU, Dying Aina M.
 ; APPLICANT: YUE, Henry
 ; APPLICANT: KHAN, Farrah A.
 ; APPLICANT: POLICKI, Jennifer L.
 ; APPLICANT: AD-YOUNG, Janice
 ; APPLICANT: YANG, Junming
 ; APPLICANT: HARLAND, Lee
 ; APPLICANT: WALSH, Rodrick T.
 ; APPLICANT: LO, Terence P.
 ; APPLICANT: BOROMSKY, Mark L.
 ; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
 ; FILE REFERENCE: PI-0044 PCT
 ; CURRENT APPLICATION NUMBER: US/10/220,382
 ; CURRENT FILING DATE: 2001-03-01
 ; PRIOR APPLICATION NUMBER: 60/186,854; 60/188,384; 60/190,453; 60/190,730
 ; PRIOR FILING DATE: 2000-03-03; 2000-03-10; 2000-03-17; 2000-03-20
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 39
 ; LENGTH: 951
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US2003011911A1 7472446CBI
 US-10-220-382-39

Query Match 83.9%; Score 819.8; DB 15; Length 951;
 Best Local Similarity 91.4%; Pred. No. 1.4e-263;
 Matches 869; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

20 ATGAGAGCTCCGGAAGCTCAGCTTGGAGAGCGGCTTCACTTGGTGGGAGTTCTGAATGAC 79
 1 ATGAGAGCTCCGGAAGCTCAGCTTGGAGAGCGGCTTCACTTGGTGGGAGTTCTGAATGAC 60
 80 AGTGGGTCTCCGGAAGCTCAGCTTGGAGAGCGGCTTCACTTGGTGGGAGTTCTGAATGAC 139
 61 AGTGGGTCTCCGGAAGCTCAGCTTGGAGAGCGGCTTCACTTGGTGGGAGTTCTGAATGAC 120
 140 AGCAATGCTCGTGGAGAGCTCAGCTTGGAGAGCGGCTTCACTTGGTGGGAGTTCTGAATGAC 199

Db 121 AGCAATGGCTACTGCTCTGGCTATACCATGGAACCGGCTCCACATGCCCTATGAC 180

QY 200 CTCCTGCTGGGAGAGCTCTCTCATGAGACCTCTGTTCACTGTTGTCACTCCAG 259

Db 181 CTCCTGCTGGGAGAGCTCTCTCATGAGACCTCTGTTCACTGTTGTCACTCCAG 240

QY 260 GCGTTGGCGGACTTTTGTGGCGAAGAAACAATATCTCTTGGAGGCTGTGCACTTCAG 319

Db 241 GCCCTTGGCGACTTTTGTGGCGAAGAAACAACATCTCTTGGAGGCTGTGCACTTCAG 300

QY 320 ATGTTCTGTGCACTGACAAATGGGTAGGGCTGAGAGACCTCTACTGGCTTCATGGCTAT 379

Db 301 ATGTTCTGTGCACTGACAAATGGGTAGGGCTGAGAGACCTCTACTGGCTTCATGGCTAT 360

QY 380 GACAGGTATGTGGCACTTTGTCAATCTCTGAAATACATGACCTCTCATGAGCCCAAGATC 439

Db 361 GACAGGTATGTGGCACTTTGTCAATCTCTGACATCATGACCTCTCATGAGCTCAAGAGCC 420

QY 440 TGTGTGATCATGTGTGGCCACATCTGGAATCTGGACATCCTGTATTTGATAGACATACC 499

Db 421 TGTGTGCTATGTTGTGGCCACAGTCTGGAATCTGGACATCCTGTATTTGATAGACATACC 480

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Db 481 GTGTATACATGACATCATCTCTCTGTGAGGGCCCAAGAAATACAGGATCTTCTCTGTGAG 540

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Db 601 GTGATGGGTGTGACTTCTCTGTGATTCCTCTTGTGTGTATTTGTGGCTCTCTATACACA 660

QY 680 GTCCATATCATGTGTCTTGTATGTCATTAATATGAGGGAGAGAAAGCCCTTGTACCC 739

Db 661 ATTCTACTCATGTGTCTCTCATATGTCATTAATATGAGGGAGAGAAAGCCCTTGTACCC 720

QY 740 TGTCTTTCACACCTGATTTGTGTGGAGATGTTCTATGAGAGCTGGCAATTCATATGATATC 799

Db 721 TGTCTTTCACACCTGATTTGTGTGGAGATGTTCTATGAGAGCTGGCAATTCATATGATATC 780

QY 800 TTGCCAGTTCCTTTCACAGAGCCCAACAAGACAATCATATCTCTGTTTCTACACAATT 859

Db 781 TTGCCAGTTCCTTTCACAGAGCCCAACAAGACAATCATATCTCTGTTTCTACACAATT 840

QY 860 GTCACTCCAGCCCTGAAATCCCATCTCATACAGCTGAGGAATAGAGAGTCAATGCGGCC 919

Db 841 GTCACTCCAGCCCTGAAATCCCATCTCATACAGCTGAGGAATAGAGAGTCAATGCGGCC 900

QY 920 TTGAGAGAGGTCTCTGGAGAAATATACATCGGCTGGACATTCACAGCTCTAG 970

Db 901 TTGAGAGAGGTCTCTGGAGAAATATACATCTGCGCAGACATCTCACGCTCTAG 951

RESULT 15
US-10-300-846-25
Sequence 25, Application US/10300846
Publication No. US20030207337A1
GENERAL INFORMATION:
APPLICANT: HAN, YI
APPLICANT: ZOZULYA, SERGEY
APPLICANT: BOHEVERRI, FERNANDO
APPLICANT: WANG, KUN
TITLE OF INVENTION: OLFACTORY RECEPTORS FOR ISOVALERIC ACID AND RELATED
TITLE OF INVENTION: MALODORANTS AND USE THEREOF IN ASSAYS FOR
FILE REFERENCE: 078003-0291924
CURRENT APPLICATION NUMBER: US/10/300,846
CURRENT FILING DATE: 2002-11-21
PRIORITY APPLICATION NUMBER: 60/348,371
PRIORITY FILING DATE: 2002-01-16

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; PRIOR APPLICATION NUMBER: 09/809,291
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/341,872
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 951
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-300-846-25

Query Match      83.9%   Score 819.8;   DB 16;   Length 951;
Best Local Similarity 91.4%;   Pred. No. 1.4e-26;
Matches 869; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

```

QY	20	ATGAGAGCTCGGAACTCCACCTTGAGGAAGGGCTTACTTGGTGGGGAATCTGAAATGAC	79
Db	1	ATGAGAGCTCGGAACTCCACCTTGAGGAAGGGCTTACTTGGTGGGGAATCTGAAATGAC	60
QY	80	AGTGGGCTCTCTGAATCTGCTCTATGCTTACAATTTTACAATCTTATACATGTTGGACTGAC	13
Db	61	AGTGGGCTCTCTGAATCTGCTCTATGCTTACAATTTTACAATCTTATACATGTTGGACTGAC	12
QY	140	AGCAATGATGTGTCGCTCTGGGCATACCATAGAAACCCGGCTCCACATGCCCCATGATAC	19
Db	121	AGCAATGATGTGTCGCTCTGGGCATACCATAGAAACCCGGCTCCACATGCCCCATGATAC	18
QY	200	CTTCCTGCTTGGGAGCTCTCTCATGAGACCTCTCTTTCACATCTGTTTGACTCCCCAG	25
Db	181	CTTCCTGCTTGGGAGCTCTCTCATGAGACCTCTCTTTCACATCTGTTTGACTCCCCAG	24
QY	260	GCTTTGGCGGACCTTTCTGGCGAGAAACACTATCTCTTTGGAGGCTGCACTTGAC	31
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QY	320	ATGTTCTCTGGACATGACAAATGGGTAGCGGCTGAGAGACCTCTACCTGGCTTCATGGCCAT	37
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QY	380	GACAGGATATGTGGCCATTTGTCACTCTTGAAATACATGACCCCTCATAGAGCCCAAGATC	43
Db	361	GACAGGATATGTGGCCATTTGTCACTCTTGAAATACATGACCCCTCATAGAGCCCAAGATC	42
QY	440	TGCTGATATATGTGGCCACATCTTGATCTTGATCTGATCTGATATGACATATAC	49
Db	421	TGCTGATATATGTGGCCACATCTTGATCTTGATCTGATCTGATATGACATATAC	48
QY	500	ATGTACACTATGACACCTCCCTTCTGTGTCTCTGGGAAATACAGGACATCTGCTGTGAG	55
Db	481	ATGTACACTATGACACCTCCCTTCTGTGTCTCTGGGAAATACAGGACATCTGCTGTGAG	54
QY	560	ATCCCACTCTTGCTGAAGTTGGCTGTGCTGATACCTCCAGATGAGCTTATATATAC	61
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QY	620	GTTGACAGGATGACTTCTCTCTTGCTCCCATTTTGCGCAATGTTGGCTGCTTACACCTA	67
Db	601	GTTGACAGGATGACTTCTCTCTTGCTCCCATTTTGCGCAATGTTGGCTGCTTACACCTA	66
QY	680	GTTCTATTTCACGTGCTTGATGATGCCATCAATGAGGGGAGAAAGAGCCCTGTGCACC	73
Db	661	GTTCTATTTCACGTGCTTGATGATGCCATCAATGAGGGGAGAAAGAGCCCTGTGCACC	72
QY	740	TGCTTTTCCACCTGATGTTGGTTCGGGATGTTCTATGAGAGCTGCCACATTCATGATGTC	79
Db	721	TGCTTTTCCACCTGATGTTGGTTCGGGATGTTCTATGAGAGCTGCCACATTCATGATGTC	78
QY	800	TTGCCAGATCTCTTCACAGGCCCAACAGACATCATCTGTGTTTCTTACACAAT	85
Db	781	TTGCCAGATCTCTTCACAGGCCCAACAGACATCATCTGTGTTTCTTACACAAT	84
QY	860	GTCATCTCAGCCCTGATATCCACTATCTTACAGCCTTGAGGATATGAGAGGTCAATCGGGCC	91

Db 841 GTGACTCCAGCCCTGTAATCCACTCATCTTACAGGCTGAGGATTAAGSAGGTCAATGCGGCC 900
QY 920 TTGAGGAGGGGTCTCTGGAAAAATACATATCTGCTGGCAATTCCAGCTCTAG 970
Db 901 TTGAGGAGGGGTCTCTGGAAAAATACATGCTGCGACACACTCCAGGCTCTAG 951

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Job time : 511 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 22, 2004, 12:56:50 ; Search time 3874 Seconds

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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41: em_hgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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5	936	95.8	947	6	AX241682 Sequence
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9	835	85.5	171660	2	AC017103 Homo sapi
10	835	85.5	173611	9	AC087280 Homo sapi
11	835	85.5	211735	9	AC091564 Homo sapi
12	834	85.4	1008	6	AX210250 Sequence
13	834	85.4	1008	6	AX551018 Sequence
14	832.4	85.2	1008	6	AX551020 Sequence
15	819.8	83.9	951	6	AX244613 Sequence
16	819.8	83.9	951	6	AX448455 Sequence
17	819.8	83.9	951	6	BD144532 Novel G-P
18	816.8	83.6	948	6	AX241679 Sequence
19	701.8	71.8	948	4	AY355744 Canis fam
20	683.2	69.9	155781	2	AF321234 Mus muscu
21	683.2	69.9	269821	2	AC137524 Mus muscu
22	679.6	69.6	951	10	AY317827 Mus muscu
23	678.2	69.4	194280	10	AC116327 Mus muscu
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25	678.2	69.4	269821	2	AY073740 Mus muscu
26	674.4	69.4	239821	2	AC098982 Rattus no
27	674.4	69.4	239821	2	AC098982 Rattus no
28	672.6	68.8	257621	2	AC094703 Rattus no
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30	671	68.7	951	10	AY073025 Mus muscu
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40	638	65.3	649	9	AF399487 Homo sapi
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42	636.6	65.2	948	10	AY073499 Mus muscu
43	636.6	65.2	948	10	AY317816 Mus muscu
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ALIGNMENTS

RESULT 1
LOCUS AX686711 977 bp DNA linear PAT 29-MAR-2003
DEFINITION Sequence 1 from Patent WO02070707.
ACCESSION AX686711
VERSION AX686711.1 GI:29372291
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
AUTHORS Padigaru,M., Gerlach,V.L., Smithson,G., Stone,D., Bin-Yang,R.,
Conley,P., Hart,M., Tomlinson,J.E., Topper,J.N., Kekuda,R.,
Casman,S.U., Edinger,S. and MacDougall,J.R.

TITLE Gpcr-like proteins and nucleic acids encoding same
JOURNAL Patent: WO 02070707-A 1 12-SEP-2002;
Coragen Corporation (US); COR THERAPEUTICS, INC. (US)
FEATURES Location/Qualifiers
source 1..977
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 977; DB 6; Length 977;
Best Local Similarity 100.0%; Pident. No. 1,3e-279;
Matches 977; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 GCACCTTAAAAAACAATCATGAGCTCCGGAATCCACCTTGGAGGCGCTTCACTT 60
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61 GGTGGGATTTCTGAATGACAGTGGGCTCTCTGAAGTCTCTATGCTATCAATCAT 120
121 ATACATGTTGGCACTGACAGCAATGGTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
121 ATACATGTTGGCACTGACAGCAATGGTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
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541 CAGGACATCTGCTCTGATGATCCACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600
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841 CTCTGTTTCTTACCAATTTGTCACCTCCAGCCCTGATTCACATCTCTCTCTCTCT 900
841 CTCTGTTTCTTACCAATTTGTCACCTCCAGCCCTGATTCACATCTCTCTCTCTCT 900

QY 901 TAAAGAGTCATGCGGCGCTTGAAGAGGCTCTGGGAAAAATPACTACTGTCACATTC 960
DB 901 TAAAGAGTCATGCGGCGCTTGAAGAGGCTCTGGGAAAAATPACTACTGTCACATTC 960
QY 961 CACGCTCTAGGAAGA 977
DB 961 CACGCTCTAGGAAGA 977

RESULT 2
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LOCUS Homo sapiens chromosome 11, clone RP11-732A19, complete sequence.
DEFINITION AC091564
AC091564.12 GI:22657585
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 211735)
2 (bases 1 to 211735)
Unpublished
Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S.,
Barra, N., Basteien, V., Boguslavsky, L., Bouckhelter, B., Brown, A.,
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Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W.,
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TITLE
JOURNAL
REFERENCE
Submitted (07-MAY-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
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Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
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TITLE
JOURNAL
REFERENCE
Submitted (13-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 211735)

AUTHORS

Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barina, N., Bastien, V., Bloom, T., Boguski, L., Bouckgeater, B., Camarata, J., Chang, J., Chazaro, B., Choquet, Y., Collymore, A., Cook, A., Cooke, P., DeArnell, K., Dewar, K., Diaz, J.S., Dodge, S., Fero, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardina, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Holme, M., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karas, A., Kelle, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrum, J., Meneses, L., Minova, T., Mlewa, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Nobu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunhkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupack, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Teifaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Vel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zambek, L., Zimmer, A. and Zody, M.

TITLE

JOURNAL

Submitted (03-SEP-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Sep 3, 2002 this sequence version replaced gi:22123080.

COMMENT

All repeats were identified using RepeatMasker:

Smith, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: MIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence.submissions@genome.wi.mit.edu

Project Information

Center project name: L11860

Center clone name: 732_A_19

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VERSION	KEYWORDS
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SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 Suwa,M., Sato,T., Okouchi,I., Arita,M., Futami,K., Matsumoto,S., Tsuchimi,S., Aburatani,H., Asai,K. and Akizawa,Y. Genome-wide discovery and analysis of human seven transmembrane helix receptor genes Unpublished 2 (bases 1 to 1350) Suwa,M.
JOURNAL	Direct Submission Submitted (11-JUL-2001) Makiko Suwa, Computational Biology Research Center (CBRC), National Institute of Advanced Industrial Science and Technology (AIST); 2-41-6 Aomi Koto-ku, Tokyo 135-0064, Japan (E-mail:m-suwa@aist.go.jp; URL:http://www.cbrc.jp/, Tel:81-3-3599-8080, Fax:81-3-3599-8081)
AUTHORS	This sequence is a seven transmembrane helix receptor candidate predicted from the whole human genome sequences using our automatic system that contains programs of gene finding(genepecder), sequence search, motif-domain assignment and transmembrane helix prediction. And the sequence is submitted by the collaborative project between [Computational Biology Research Center (CBRC), National Institute of Advanced Industrial Science and Technology (AIST)] and [genome Science Division, Research Center for Advanced science and Technology (RCAST), University of Tokyo].
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 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 208430)
 AUTHORS Waterston, R.H.
 TITLE The sequence of Homo sapiens clone
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 208430)
 AUTHORS Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (30-MAR-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
 COMMENT On Jun 17, 2000 this sequence version replaced gi:7344780.

Sequencing vector: M13; 98%
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 Chemistry: Dye-primer; 98% of reads
 Chemistry: Dye-terminator; Big Dye; 2% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 198825 bases at least Q40
 Consensus quality: 202103 bases at least Q30
 Consensus quality: 203934 bases at least Q20
 Insert size: 219000; agarose-fp
 Quality coverage: 4.27 in Q20 bases; agarose-fp
 Quality coverage: 4.55 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 18 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

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QY      181 GCTCCACATGCCCATGTAACCTCTGCTGGGACGCTCTCTCATAGAACCTCTGTTAC 240
DB      52449 GCTCCACATGCCCATGTAACCTCTGCTGGGACGCTCTCTCATAGAACCTCTGTTAC 52390
QY      241 ATCTGTTGACCTCCGAAGGCTTGGCGGACCTTTCGCGAGAGAAACATATCTTCCTT 300
DB      52389 ATCTGTTGACCTCCGAAGGCTTTCGCGAGAGAAACATATCTTCCTT 52331
QY      301 TGAAGGCTGGCACTTCAAGATGTTCCGCACTGACAAATGGTAGGCTGAGACCTCTT 360
DB      52330 TGAAGGCTGGCACTTCAAGATGTTCCGCACTGACAAATGGTAGGCTGAGACCTCTT 52271
QY      361 ACTGGCCTTATGAGGCTATGAGAGTATGAGGCAATTTGTCATCTCTGAAATACATGAC 420
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QY      481 GATTGCTATGAGACATACATGATGACATATGACATCTCCCTTTCTGATGCTGGAAAT 540
DB      52150 GATTGCTATGAGACATACATGATGACATATGACATCTCCCTTTCTGATGCTGGAAAT 52091
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DB      52090 CAGGCACTGCTCTGTAGATATCCACCTTGCTGAAAGTTGGCTGTGCTGATATCTCAG 52031
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DB      51970 TGTGGCTCTTACACACTGATGCTTATTCATGCTGCTGCTGATATGTCATCAATAGAGGGAG 51911
QY      721 GAAGAAAGCCCTTTCACCTGCTCTTCCACCTGATATGCTGCGGATGTTCTATAGAGC 780
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QY      781 TGCCACATTCATGATATGCTTTCGCCAGTTCTCTTCCACAGCCCAACAGCAACATATAT 840
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DB      51790 CTGCTTTTCTACACATTTGTCATCTCCAGCCCTGAATTCATCTATCAGCTGAGGAA 51731
QY      901 TAAGGAGTCATAGCGGCTTGAAGAGGCTCTGCGGAAATATACATATGCTGGACATTC 960
DB      51730 TAAGGAGTCATAGCGGCTTGAAGAGGCTCTGCGGAAATATACATATGCTGGACATTC 51671
QY      961 CACGCTTAGGGAAGA 977
DB      51670 CACGCTTAGGGAAGA 51654

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RESULT 5

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AX241682      947 bp      DNA      linear      PAT 26-SEP-2001
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

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TITLE
JOURNAL
FEATURES
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Best Local Similarity 99.9%; Pred. No. 2.1e-267;
Matches 947; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      20 ATGAGACTCCGGAACCTCCACCTTGGGAAGCGGCTTCATCTTGGTGGGATTTGAAATGAC 79
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QY      80 AGTGGCTCTCTGAACTGCTCTATGCTACATTTTAACTATATCATGTTGGCACTGACC 139
DB      61 AGTGGCTCTCTGAACTGCTCTATGCTACATTTTAACTATATCATGTTGGCACTGACC 120
QY      140 AGCAATGCTGCTGCTCTCTGCGCATACATAGAAACCCGCGCTCCGACATGCCATGAC 199
DB      121 AGCAATGCTGCTGCTCTCTGCGCATACATAGAAACCCGCGCTCCGACATGCCATGAC 180
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Db 241 GCTT- GCGGACTTTCTGGGAGAGAAAACATATCTCTTTGAGAGCTGTGACTTCA 299
Qy 320 ATGTTCTGGGAGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 379
Db 300 ATGTTCTGGGAG 359
Qy 380 GACAGATATGAG 439
Db 360 GACAGATATGAG 419
Qy 440 TCTGATATGAG 499
Db 420 TCTGATATGAG 479
Qy 500 ATGACACTATGAG 559
Db 480 ATGACACTATGAG 539
Qy 560 ATCCACCTTGTGAG 619
Db 540 ATCCACCTTGTGAG 599
Qy 620 GTGACAGTGTGAG 679
Db 600 GTGACAGTGTGAG 659
Qy 680 GTCCATTCAG 739
Db 660 GTCCATTCAG 719
Qy 740 TGTCTTCCAG 799
Db 720 TGTCTTCCAG 779
Qy 800 TTGCCAGTCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 859
Db 780 TTGCCAGTCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 839
Qy 860 GTCACTCAG 919
Db 840 GTCACTCAG 899
Qy 920 TTGAG 967
Db 900 TTGAG 947

RESULT 6
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LOCUS AX210248
DEFINITION Sequence 8 from Patent W00157215.
ACCESSION AX210248
VERSION AX210248.1 GI:15424570
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukavoda; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Padigaru, M., Spytek, K. A., Li, L., Ballinger, R. A., Mishra, V. S. and Baumgartner, J. C.
TITLE Novel polypeptides and nucleic acids encoding same
JOURNAL Patent: WO 0157215-A 8 09-AUG-2001;
Curagen Corporation (US)
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ORIGIN /db_xref="taxon:9606"

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Best Local Similarity 91.2%; Pred. No. 2,7e-237;
Matches 886; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

Qy 7 AAAAAACATCATGAG 66
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Qy 127 GTTGGACATGAG 186
Db 179 GTTGGACATGAG 238
Qy 187 CATGCCATGAG 246
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Db 299 TGTCACTCCAG 358
Qy 307 CTGAGCACTTGAAG 366
Db 359 CTGAGCACTTGAAG 418
Qy 367 CTTCATGAG 426
Db 419 CTTCATGAG 478
Qy 427 GAGCCCAAG 486
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Qy 487 TATGAG 546
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Qy 667 CTGCAACAG 726
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Qy 847 TTTCTACAG 906
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Qy 967 CTGAG 977

Db 1019 CTAGGAGAGA 1029

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LOCUS
DEFINITION Sequence 275 from Patent EP1270724.
ACCESSION AX646083
VERSION AX646083.1 GI:28798462
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
1 Suwa,M., Asai,K., Akiyama,Y. and Aburatani,H.
AUTHORS Guanosine triphosphate-binding protein coupled receptors
TITLE Patent: EP 1270724-A 275 02-JAN-2003;
JOURNAL National Institute of Advanced Industrial Science and Technology
(JIP) Center for Advanced Science and Technology Incubation, Ltd.
(JIP)

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CDS

ORIGIN

Query Match 85.5%; Score 835; DB 6; Length 1351;
Best Local Similarity 91.2%; Pred. No. 2.8e-237;
Matches 886; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 7 AAAAAACATCATGAGAGCTCCGGAATCCACTGGGAAAGGCGCTTCACTGGTGGG 66
DB 188 AAGAAACACAGCATGAGAGCTCCGGAATCCACTGGGAAAGGCGCTTCACTGGTGGG 247
QY 67 GATTGAGATGACAGAGGGGTCTCTGAAGCTCTCTATGCTACATTACATCTTATACAT 126
DB 248 GATTGAGATGACAGAGGGGTCTCTGAAGCTCTCTATGCTCTGTCTCAATTCATCTTATACAT 307
QY 127 GTTGGACAGTACAGCAATGAGTGTCTGCTCTCTGGCCATCATCAATGAAAGCCGGCTCCA 186
DB 308 GTTGGCCCTGATCAGCAATGAGTGTCTGCTCTCTGGCCATCATCAATGAAAGCCGGCTCCA 367
QY 187 CATGCCATGATCTCTGCTCTGGGAGCTCTCTCTCAATGAGAGCTCTGTTCAATCTGT 246
DB 368 CATGCCATGATCTCTGCTCTGGGAGCTCTCTCTCAATGAGAGCTCTGTTCAATCTGT 427
QY 247 TGTCACTCCCAAGGCTTGGCGGACTTCTGCGCAGAGAAACATCTCTCTTGGAGG 306
DB 428 TGTCACTCCCAAGGCTTGGCGGACTTCTGCGCAGAGAAACATCTCTCTTGGAGG 487
QY 307 CTGTGACATTCAGATGTTCTCTGCGACATGACATGAGTGGCTGAGAGACTCTCTACTGGC 366
DB 488 CTGTGACATTCAGATGTTCTCTGCGACATGACATGAGTGGCTGAGAGACTCTCTACTGGC 547
QY 367 CTTCATAGGCTTATGACAGATGAGTGGCTTGTGCAATCTCTGAAATATGACATCTCAT 426
DB 548 CTTCATAGGCTTATGACAGATGAGTGGCTTGTGCAATCTCTGCAATATGACATCTCAT 607
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Db 608 GAGCTCAAGAGCGCTGCTGCTCATGAGGCGACGCTCTGATCTCTGATCTCTTAAGTGC 667
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DB 668 CTATATATATCCGTGATATACATGACATATCTCTCTGAGAGGCGCCAGAGATCAGGCA 727
QY 547 TCTGCTGTGAGATCCACCTCTGAGAGTGGCTGTGCTGATATCTCTTCAAGTATGA 606
DB 728 TCTTCTGTGAGATCCACCTCTGAGAGTGGCTGTGCTGATATCTCTTCAAGTATGA 787
QY 607 GCTATATATATACGTGACAGTGTGACCTCTCTGCTGCTCCCATTTCTGCAATGAGGC 666
DB 788 GCTATGATATATGATGAGTGTGACCTCTCTGATCTCTCTGCTGCTTATCTGCGC 847
QY 667 CTCTACACATGATCTCTATCTACCTGCTCTGATGCTGATGCTCAATGAGGAGGAGAGA 726
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QY 727 AGCCCTGTGACCTGCTCTCTCCACCTGATGCTGCTGAGATGTTCTATGAGAGCTGCCAC 786
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QY 787 ATTATGATATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 846
DB 968 ATTATGATATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1027
QY 847 TTTTACACAAATTTGCTACCTGACCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 906
DB 1028 TTTTACACAAATTTGCTACCTGACCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1087
QY 907 GGTATGCGGGGCTTGGAGAGGCTCTCTGAGAAATATGCTGCTGCTGCTGCTGCTGCT 966
DB 1088 GGTATGCGGGGCTTGGAGAGGCTCTCTGAGAAATATGCTGCTGCTGCTGCTGCTGCT 1147
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RESULT 8
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LOCUS
DEFINITION Homo sapiens gene for seven transmembrane helix receptor, complete
cds, isolate:CBRCWTM_386.
AB065823
AB065823.1 GI:21928911
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
1 Suwa,M., Sato,T., Okouchi,I., Arita,M., Futami,K., Matsumoto,S.,
AUTHORS Tsutsumi,S., Aburatani,H., Asai,K. and Akiyama,Y.
TITLE Genome-wide discovery and analysis of human seven transmembrane
helix receptor genes
JOURNAL Unpublished
REFERENCE
AUTHORS Suwa,M.
TITLE Direct Submission
JOURNAL
2 (bases 1 to 1351)
COMMENT
Submitted (11-JUL-2001) Makiko Suwa, Computational Biology Research
Center (CBRC), National Institute of Advanced Industrial Science
and Technology (AIST); 2-41-6 Aomi Koto-ku, Tokyo 135-0064, Japan
(E-mail:m-suwa@aist.go.jp, URL:http://www.cbrc.jp/,
Tel:81-3-3599-8080, Fax:81-3-3599-8081)
This sequence is a seven transmembrane helix receptor candidate
predicted from the whole human genome sequences using our automated
system that contains programs of gene
finding (GenDecoder), sequence search, motif-domain assignment and
transmembrane helix prediction.
And the sequence is submitted by the collaborative project between
[Computational Biology Research Center (CBRC), National Institute

CDS

ORIGIN

Query Match	85.5%;	Score 835;	DB 9;	Length 1351;
Best Local Similarity	91.2%;	Pred. No. 2.8e-237;		
Matches 886;	Conservative 0;	Mismatches 85;	Indels 0;	Gaps 0

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Db	308	GTTGGCCCTGAATCAAGCAATGAGCCCTACTGTCTCTGACTATCAACATGAAAGCCGGCTCA	367
QY	187	CATGCCCATGTACTCTCTGCTGGGACGCTCTCTCAATGAAACCTCGTTCAACTCTGT	246
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QY	247	TGTGACTCCCAAGGCTCTGGGGAATTTCTGTGGCAGAGAAAAACAATTCTCCTTGGAGG	306
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QY	307	CTGTGCACATTAGATGTTCTGTGGCACTGACAAATGGGTAGCGCTGAGACCTCTACTGGC	366
Db	488	CTGTGCCCTTACAGATGTTCTGTGGCACTGACAAATGGGTAGCGCTCTACTGGC	547
QY	367	CTTCATGGCCTATGACAGGTAATGTGGCCATTGTTCATCCTCTGAAATACATGACCCCTAT	426
Db	548	CTTCATGGCCCTATGACAGGTAATGTGGCCATTGTTCATCCTCTGACATACATGACCCCTAT	607
QY	427	GAGCCCAAGAGCTGCTGGATCATGTGGGCGCAACTCCGGAATCCTTGGCATCTCCGATTGC	486
Db	608	GAGCTCAAGAGCCTGCTGGCTCAATGTGGCGCAAGTCTCGAATCCTCGAATCCCTAAATGTC	667
QY	487	TATAGCAATACCAATGTAACAATTGCACTTCCCTTCTGTGTGTGCTGTGGAAATCAGGCA	546
Db	668	CCATATATATACCGTATATACCAATGCACTATCCCTTCTGTGAGGGCCCAAGAGATCAAGCA	727
QY	547	TCTGCTCTGAGATATCCCACTTGGCTGGAAGTTGGCTGTGATATACCTTCCAGATATGA	606
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QY	607	GCTTATATAATATACCTGACAGGTGTGACTTTCTCTTCTGCCAATTTCTGCATTTGGGC	666
Db	788	GCTCATGATATATGTGATGGGTGTGACCTTCTGATTCCTCTCTTGTCTGTATATCTGGC	847
QY	667	CTCCTAACACATAGTCCCTATTTCACTGTGCTTCTGTATGCCATCAAAATGAGGGAGAAAGAA	726

Accession	Sequence	Position
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QY	ATTCAATGATGCTTGGCCAGTTCCTTCCACAGCCCCAAACAAGCAACATCATTTCTGT	846
D8	ATTCAATGATGCTTGGCCAGTTCCTTCCACAGCACCAAGAACCAACATCATTTCTGT	1027
QY	TTTCTACCAATTGTCACTCCAGGCTTAATCCACTCATCTACAGCCTGAGAAATAAGA	906
D8	TTTCTACCAATTGTCACTCCAGGCTTAATCCACTCATCTACAGCCTGAGAAATAAGA	1087
QY	GGTCAATGGGGCCTTTGAGAGGGTTCCTGGAAAAATACATCTGCTGGCACATTCACGCT	966
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D8	CTAGGGAAAGA 1158	

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VERSION	AC017103
KEYWORDS	AC017103.5 GI:9838275
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ORGANISM	Homo sapiens (human)
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REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 171660) Waterston,R.H. The sequence of Homo sapiens clone Unpublished 2 (bases 1 to 171660) Waterston,R.H. Direct Submission Submitted (09-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA On Aug 17, 2000 this sequence version replaced gi:8570316.
COMMENT	

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----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H NH0560B16
Summary Statistics
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Sequencing vector: MJ3, 70x
Sequencing vector: plasmid, 30x
Chemistry: Dye-primer ET, 70x of reads
Chemistry: Dye-terminator Big Dye, 30x of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 161395 bases at least Q40
Consensus quality: 165413 bases at least Q40
Consensus quality: 167520 bases at least Q30
Insert size: 161000; agarose-fp
Insert size: 171320; sum-of-coverage
Quality coverage: 4.44 in Q20 bases; agarose-fp
Quality coverage: 4.17 in Q20 bases; sum-of-coverage
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 16 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.

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* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1723: contig of 1723 bp in length
* 1724 1823: gap of unknown length
* 1824 4819: contig of 2996 bp in length
* 4820 4919: gap of unknown length
* 4920 8082: contig of 3163 bp in length
* 8083 8183: gap of unknown length
* 8183 11955: contig of 3773 bp in length
* 11955 12056: gap of unknown length
* 12056 15446: contig of 3391 bp in length
* 15447 15547: gap of unknown length
* 15547 19581: contig of 4034 bp in length
* 19581 25959: gap of unknown length
* 25959 33385: contig of 6278 bp in length
* 33385 33485: gap of 7327 bp in length
* 33486 42561: gap of unknown length
* 42562 54313: gap of 11652 bp in length
* 54314 72085: contig of 17672 bp in length
* 72086 89296: gap of unknown length
* 89297 89397: contig of 17111 bp in length
* 89397 104805: gap of unknown length
* 104806 121851: contig of 15409 bp in length
* 121852 121951: gap of unknown length
* 121952 141389: contig of 16946 bp in length
* 141390 141489: gap of unknown length
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FEATURES

source

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Query Match 85.5%; Score 835; DB 2; Length 171660;
Best Local Similarity 91.2%; Pred. No. 5.1e-237;
Matches 886; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

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Db 80242 TGTCACCTCCAGAGGCTTGGGAGCTTTCTGCGAGAGAAAACATATCTCT 80183
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Db 80182 CTGTCACCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 80123
Qy 367 CTTCAATGCGCATGACAGATGATGATGATGATGATGATGATGATGATGATG 426
Db 80122 CTTCAATGCGCATGACAGATGATGATGATGATGATGATGATGATGATG 80063
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Db 80002 CTTATATATATACCGATATACATGATGATGATGATGATGATGATGATG 79943
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Db 79942 TCTGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 79883
Qy 607 GCTTATATATAGATGATGATGATGATGATGATGATGATGATGATGATGAT 666
Db 79882 GCTTATATATAGATGATGATGATGATGATGATGATGATGATGATGATG 79823
Qy 667 CTCTTACACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 726
Db 79822 CTCTTATTAACAATTTACTACTGATGATGATGATGATGATGATGATGAT 79763
Qy 727 AGCCCTTGTCACTGCTTCCACCTGATGATGATGATGATGATGATGATGATG 786
Db 79762 AGCCCTTGTCACTGCTTCCACCTGATGATGATGATGATGATGATGATG 79703
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ACCESSION AC087280
VERSION   AC087280.11  GI:17223193
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
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AUTHORS  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Euteria; Primates; Catarrhini; Hominidae; Homo.
          1 (bases 1 to 173611)
          Birren, B., Linton, L., Nusbaum, C. and Lander, E.
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          Homo sapiens chromosome 11, clone RP11-560B16
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          Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S.,
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          Research, 320 Charles Street, Cambridge, MA 02141, USA
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          Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
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          Submitted (01-DEC-2001) Whitehead Institute/MIT Center for Genome
          Research, 320 Charles Street, Cambridge, MA 02141, USA
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Center: Whitehead Institute/ MIT Center for Genome Research

Center code: MIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

Project Information

Center project name: L11843

Center clone name: 560_B_16

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DEFINITION	Sequence 10 from Patent WO0157215.				
ACCESSION	AX210250				
VERSION	AX210250.1				
KEYWORDS	GI:15424571				
SOURCE					
ORGANISM	Homo sapiens (human)				
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	Eumetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 Padigaru,M., Spytek,K.A., Li,L., Ballinger,R.A., Mishra,V.S. and Baungartner,J.C				
AUTHORS	Novel polypeptides and nucleic acids encoding same				
JOURNAL	Patent: WO 0157215-A 10 09-AUG-2001;				
FEATURES	Cutagen Corporation (US)				
	Location/Qualifiers				

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ACCESSION AX551020
VERSION AX551020.1 GI:25814025
KEYWORDS

SOURCE
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euteria; Primates; Catarrhini; Hominidae; Homo.

TITLE
1 Alsbrook, J.P., Burgess, C.E., Grose, W.M., Lepley, D.M., Padigaru, M.
and Spytek, K.A.

JOURNAL
Novel single nucleotide polymorphisms for olfactory receptor-like
polypeptides and nucleic acids encoding the same
Patent: WO 0236632-A 13 10-MAY-2002;
Curagen Corporation (US)

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ACCESSION AX244613
VERSION AX244613.1 GI:15859514
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Lal, P., Tang, Y.T., Patterson, C., Yao, M.G., Shih, L.L.,
Tribouley, C.M., Lu, D.A., Yue, H., Khan, F.A., Policky, J.L.,
Au-Yang, J., Yang, J., Harland, L., Walsh, R.T., Lo, T.P. and
Borowsky, M.L.
TITLE G-protein coupled receptors
JOURNAL Patent: WO 0166742-A 39 13-SEP-2001;
Incyte Genomics, Inc. (US)
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5	241	24.7	1411	4	US-09-524-730-3
6	237.4	24.3	966	3	US-08-748-506-8
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12	226.4	23.4	966	4	US-09-524-730-1
13	226.4	22.9	1351	4	US-08-748-506-6
14	223.6	22.9	1351	4	US-09-546-986A-5
15	223.6	22.9	1351	4	US-09-524-730-5
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18	213.2	21.8	1990	4	US-09-016-434-1056
19	212.4	21.7	1713	2	US-08-467-948A-1
20	212.4	21.7	1713	3	US-08-467-947A-1
21	212.2	21.7	1283	4	US-09-016-434-1413
22	209.4	21.4	669	4	US-09-465-901-23
23	208.2	21.3	1062	4	US-09-668-680-10
24	207.8	21.3	669	4	US-09-465-901-19
25	207.4	21.3	669	4	US-09-465-901-27
26	202.4	20.7	1297	4	US-09-668-680-11
27	198	20.3	3459	4	US-09-016-434-1363

28	190.6	19.5	945	4	US-09-016-434-1114	Sequence 1114, Ap
29	190.4	19.5	669	4	US-09-465-901-13	Sequence 13, Appl
30	189.4	19.4	669	4	US-09-465-901-11	Sequence 11, Appl
31	188.4	19.3	1438	4	US-09-016-434-1313	Sequence 1313, Ap
32	184.6	18.9	1080	4	US-09-668-680-9	Sequence 9, Appl
33	182	18.6	669	4	US-09-465-901-41	Sequence 41, Appl
34	177.2	18.1	669	4	US-09-465-901-31	Sequence 31, Appl
35	176.2	18.0	900	3	US-09-085-371-5	Sequence 5, Appl
36	174.2	17.8	681	4	US-09-465-901-29	Sequence 29, Appl
37	170	17.4	675	4	US-09-465-901-43	Sequence 43, Appl
38	168.6	17.3	648	4	US-09-016-434-1374	Sequence 1374, Ap
39	165	16.9	678	4	US-09-465-901-45	Sequence 45, Appl
40	164.8	16.9	669	4	US-09-465-901-25	Sequence 25, Appl
41	161.6	16.5	669	4	US-09-465-901-15	Sequence 15, Appl
42	161.6	16.5	669	4	US-09-465-901-35	Sequence 35, Appl
43	161.2	16.5	675	4	US-09-465-901-17	Sequence 17, Appl
44	150.4	15.4	669	4	US-09-465-901-37	Sequence 37, Appl
45	146.6	15.0	542	4	US-09-016-434-627	Sequence 627, Ap

ALIGNMENTS

RESULT 1
US-08-827-291A-1
Sequence 1, Application US/08827291A
Patent No. 5874243
GENERAL INFORMATION:
APPLICANT: Macina, Roberto
APPLICANT: Sacha, Ganesh
TITLE OF INVENTION: NOVEL OLRC15 RECEPTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY:
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,291A
FILING DATE: 28-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: King, William T
REGISTRATION NUMBER: 30,954
REFERENCE/DOCKET NUMBER: GP50001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5015
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1290 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-827-291A-1

Query Match 31.0% Score 302.8; DB 2; Length 1290;
Best Local Similarity 57.7%; Pred No. 5.2e-84;
Matches 541; Conservative 0; Mismatches 397; Indels 0; Gaps 0;
QY 7 AAAAAACATCATGAGCTCCGGACTCCACTTGGAGAGCGGCTTATCTTGTGGG 66

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Db      283 AACATACACATATAGGCAAGGAGAAATGACCTTCACTCCGACTTATCTTCGGG 342
Qy      67 GATTGATGACAGTGGGCTCTCTGAATGCTCTATGCTAATTTAACAATCTTATACAT 126
Db      343 AATCTTCAATACAGAGCCCAACCAACCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 402
Qy      127 GTTGGACATGACAGCAATGCTGCGCTCTGGGACATACCATAGAAAGCCGGCTCCA 186
Db      403 AGTGGCTTATGAGGAACTCTGCTGATGTTCTCTCTATCTTACTGAGACCAAGCTCCA 462
Qy      187 CATGCCATGATACCTCTGCTGCTGGGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 246
Db      463 CACCCCATATACCTCTCTCTGAGCAACCTGCTCTGATGAGCTCTCTCTCTCTCT 522
Qy      247 TGTACTCCCAAGGCTCTGGGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 306
Db      523 CACCGTACCAAGATGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 582
Qy      307 CTGTGACCTTACATGTTCTCTGACATGCAATGAGGCTGAGGAGCCCTGACTGGC 366
Db      583 TTGTGACACAAATTTCTCTATACATACATGCTGCTGCTCTGATGCTCTCTCTCT 642
Qy      367 CTTCATGCTATGACAGTATGAGCTATGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 426
Db      643 TGTATATGCTTATGACCGCTACACCTGCTCTGCTCTGCACTCTCTCTCTCTCTCT 702
Qy      427 GAGCCCAAGTCTGCTGATCATGCTGAGCACTCTCTCTCTCTCTCTCTCTCTCTCT 486
Db      703 GAGCCCTAAATTTGTGAGCTTATGACCTCTCTCTCTCTCTCTCTCTCTCTCTCT 762
Qy      487 TATGACATACCATGTAACCTATGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 546
Db      763 AATATATTATGCTGATGACCAATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 822
Qy      547 TCTGCTCTGATGATCCCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 606
Db      823 CTCTCTCTGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 882
Qy      607 GCTTATATATATAGTACAGAGTGTGACTCTCTCTCTCTCTCTCTCTCTCTCTCT 666
Db      883 AAGGTTATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 942
Qy      667 CTCTACACATACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 726
Db      943 TTCTCTAGCTGAGTATTTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1002
Qy      727 AGCCCTTGTACCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 786
Db      1003 AGCTTTACGACCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1062
Qy      787 AATCATATATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 846
Db      1063 GTTATATATATATACAGCCCAATCTGATGCTCTCTCTCTCTCTCTCTCTCTCTCT 1122
Qy      847 TTTCTACACATTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 906
Db      1123 AATCTACACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1182
Qy      907 GGTCAATGCGGCTCTGAGAGGCTCTGAGAAATATACA 944
Db      1183 AGTACACAGAGATCATGAAAGATCTCAGGAAAGGCA 1220

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RESULT 2
US-08-748-506-7
; Sequence 7, Application us/08748506
; Patent No. 6159707
; GENERAL INFORMATION:
; APPLICANT: Ronnelt et al.
; TITLE OF INVENTION: NOVEL SPERM RECEPTORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: US
; ZIP: 60601-6780
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,506
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,751
; FILING DATE: 09-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; REFERENCE/DOCKET NUMBER: 74940
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5600
; TELEFAX: 312-616-5700
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 966 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-748-506-7

Query Match      25.6%; Score 250.2; DB 3; Length 966;
Best Local Similarity 56.1%; Pred. No. 1e-67;
Matches 471; Conservative 0; Mismatches 368; Indels 0; Gaps 0;

Qy      117 TCCTATACATGTTGGACGACAGCAAGTGTCTGCTCTCTGCAATACCAATGAG 176
Db      116 TCATGTTCTAGTATCACTAAACAGAAATACCTCATAGCCCTTGCTATTTGTAACAAGTC 175
Qy      177 CCGGCTTCACATCCCAATGATCTCTGCTGGGAGCTCTCTCATAGGACCTCGT 236
Db      176 CATCTACACACCCCAATGATCTTTCTGSCCACTGTCTCTCTGAGATTGCT 235
Qy      237 TCACATCTGTTGTACCTCCCAAGGCTTTGGGCACTTCTGCGAGAGAAAACAATATCT 296
Db      236 ATACTTGTCTGTATACCAAGATGCTGAGACCTTTGAGAGGCCGAGGATCT 295
Qy      297 CTTTGGAGGCTGTGCACTTCAATGTTCTCTGSCATGACATGAGGTAGCGCTGAGACC 356
Db      296 CTTGGAGGGGTGTGCTCACAGATGTTCTTCAATTTCTTTGGATTAATCTGATGCT 355
Qy      357 TCTCTAGGCTTATAGGCTTATAGCAAGTATGAGGCAATTTGCAATCTCTGAAATACA 416
Db      356 GCTTATGAGCAATGAGCTTTTACCGCTATATATGTTATGTTCCCACTCCACTATG 415
Qy      417 TGACCTCATGAGCCCAAGAGTCTGCTGATCATAGTGGCCCAATCTCTGATCTCTGAT 476
Db      416 CAACCCGAATAGTGTGGGATATGTGCTATTTGGCAATTGTCTCAAGGGGATGGAT 475
Qy      477 CCTGATTTGTAATAGACATACCATGTAACATGACCTCCCTTCTGTGTCTGTGGG 536
Db      476 GCATGTAGTGTGTGGGACAGACCAATTTATTTCTCTTTGAAACTTGTGTGACCTGTG 535
Qy      537 AAATAGGACATCTGTCTGTGATGCCACCTGCTGAAGTGGCTGTGTATACCT 596
Db      536 AGATAGACCACTTCTTGTGATCTTCACTCTCTCTGACCTTCTGTGTGTATAT 595
Qy      597 CCAGTATGAGCTTATATATATGATGACAGGTGATCTTCTCTGTCTCTCCCAATTTCTG 656
Db      596 CCAAAATAGAGCTCCATCTTTTGTGGAGAGAGTCTGTGATATTTAGTCAATTTTAC 655

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QY	657	CCATGTGGCCCTCCACACATAGTCCCTATTCAGTGGTGGTAGCCATCAAAAGAG	716
Db	656	TGATATTTCTTCCTATGTCAGAAATTCCTGTCAGTGGCTGGAGAGCCTTCACTGAAG	715
QY	717	GGAGGAAGAAAGCCCTGTCACTGCTCTTCCCACTGATTTGGATCGGAGATGTTATG	776
Db	716	GGCGGCATTAAGCTCTCTCTACCTGTTCATCTCACTACTTGTAGTCAACCTTTCTATG	775
QY	777	GAGCTGCACATTCATGATGTGCTTGGCCCAAGTTCCTCCACAGCCCCAACAAGAACCA	836
Db	776	GCTCAACATCTGCCACACTATTGAGSTCCAAAGTCTTAGCCACTGCACAGAGGTGACAAAC	835
QY	837	TCATCTCTGTTTCTACACAAATGTTCACTCAGCCCTGTAATCCACTCATCTTACAGCCTGA	896
Db	836	TCTTGGCCCTCTTCAATACATCAGTGCATCATGTGTAATCCCATCATCTACAGCTTAA	895
QY	897	GGAAATPAAGAGGTCAATGGGGGCTTGAAGAGAGGTCTGTGGAAATAATCATATCTCTGGCA	955
Db	896	GGAAACAGAAAGTAAAGGGTGCACCTGAGAGAACTTGGGCTTGAAGAAAGTTCTTGACA	954

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US-09-465-901-39
US-09-465-901-39
Sequence 39, Application US/09465901
Patent No. 6492143
GENERAL INFORMATION:
APPLICANT: Reed, Randall
APPLICANT: Yau, King-Wai
APPLICANT: Krauthorst, Dietmar
TITLE OF INVENTION: Olfactory Receptor Expression Libraries
TITLE OF INVENTION: ad Methods of Making and Using Them
FILE REFERENCE: 001107,00105
CURRENT APPLICATION NUMBER: US/09/465,901
CURRENT FILING DATE: 2001-12-17
PRIORITY APPLICATION NUMBER: 60/112,605
PRIORITY FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 39
LENGTH: 669
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
OTHER INFORMATION: PCR primer
US-09-465-901-39

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Query Match	24.9%	Score 243;	DB 4;	Length 669;
Best Local Similarity	60.3%	Pred. No. 1.4e-65;		
Matches 402; Conservative	0;	Mismatches 265;	Indels 0;	Gaps 0;

QY	210	GGAGGCTCTCTCATGGACCTCGCTTCACTCTGTGTACTCCCAAGGCTTGCGG	269
Db	2	GTCACTTGCTTATTGACATGATGATACCTTCAACCATTTGCCCCAAATGCTAGT	61
QY	270	ACTTCTGCGCAGAGAAACACTATCTCTTTGGAGGCTGTGCACCTGATGTTCC	329
Db	62	ATTATCTTTTAGGGCAAGACTATTTCTTTGTGGATGACAGCTCAACCTTTTAT	121
QY	330	CACAGACATGGGTAGCGCTGAGGACCTCTACTGGCTTCATGCGCTATGACGATATG	389
Db	122	ACGTACACCTGTGGGAGCGGAGTTCTTTCTTTCTGGGCTCATGCGCTTATGATCGTATG	181
QY	390	TGGCCATTTGTCACTCTCTGAATATCATGACCTCATGAGCCCAAGACTCTGCGATCA	449
Db	182	TGGCATCTGGCAACCCACTGAGTACCTGTCTCATGAGCGCGGATCTGTGGATTA	241
QY	450	TGGTGGCCACATCTTGATCTCTGGCATCTCCGATGCTATAGAGACATACATGTACATA	509
Db	242	TCAATGAGGCTCTGTGTTGGGGGATTTTGGATGGCTCTCTCTCACTCCATACCA	301
QY	510	TGACCTCCCTTTCTGTGTGTCTGTGGAAATCAGGACCTGTGCTGTGATATCCACCT	569
Db	302	TGAGTTTTCCTTTCTGTGATCATGAGAGATTACCACTTTCTGTGTAGGACCTGTGCT	361

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RESULT 4
US-09-546-986A-3
Sequence 3, Application US/09546986A
Patent No. 6635741
GENERAL INFORMATION:
APPLICANT: Powers, Scott
APPLICANT: Yang, Jianping
APPLICANT: Cutler, Gene
APPLICANT: Tularik Inc.
TITLE OF INVENTION: No. 6635741e1 G-Protein Coupled Receptors
FILE REFERENCE: 018781-064720US
CURRENT APPLICATION NUMBER: US/09/546, 986A
CURRENT FILING DATE: 2002-04-30
PRIORITY APPLICATION NUMBER: US 09/524, 730
PRIORITY FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 1411
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (118)..(1113)
OTHER INFORMATION: human breast cancer amplified G-protein coupled
US-09-546-986A-3

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Query Match	24.7%	Score 241	DB 4	Length 1411
Best Local Similarity	55.3%	Pred. No.	8.9e-65	
Matches 509	Conservative	0	Mismatches 410	Indels 2
			Gaps	2

Qy	17	ATCATGAGCTCCGGAACCTCCACCTTGGAGAGCGGCTTCATCTTGGTGGGGAATTGGAAT	76
Db	115	ATTATTGGAGAAAGACAAATGCCAGTTACTACACAGGATTCATCCTGGTGGGCTTTCGAT	174
Qy	77	GACAGTGGGTCTCCGAACTGCTCATGCTTAATTAACAATCCTATACATGTTGGACATG	136
Db	175	CGGCTGGACTGAGAAAATTTCTCTTGTCTGTTATCTTGATCTTTCGACATCCGACCTCG	234
Qy	137	ACGAGCAATGCTCTGCTCTCTCTGCGACATCAACATAGAAGCCGGCTCACATGGCCATG	196
Db	235	GTGGGCAACACTGCATCATCTCTCTGTGTGTCATGAGATGTAGGCTCACACACCCATG	294
Qy	197	TACCTCTGCTTGGGAGCTCTCTCTATAGAACCTCTGTTCAACTGTGTCACTGCC	256
	295	TACTTCTTTCTTGGGAATCTGCTCTTTCTTAATCTCTCTCTTAAGCAAGCATTTGCCCT	354

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QY 257 AAGCCTTGGGAGCTTTCGCGAGAGAAAACATATCTCTTTGGAGGCTGTGCACTT 316
DB 355 CAGTGTCTGTGAACTTGGGGGCTTCAGAGAAACATACCTACACAGGCTGTGTGGCC 414
QY 317 CAGATGTTCTGTGCACTGACATAGGATAGCGCTGAGGACCTCTTACTGCGCTTCATGGCC 376
DB 415 CAACCTTACATCTACATATGATGTGGGCTCCACGAGTGCGTCTCTGTGTGTATGTCC 474
QY 377 TATGACAGATATGTGGCCATTTGTATCTCTGAAATATCATGACCTTATGAGCCCAAGA 436
DB 475 CATGACCCCTATGTGGCGGTCTGCGCGTCCCTGCACTACATGCAAGTATCGGCCACAT 534
QY 437 GTGTGCTGAATCATGTGGGCAACATCTGTGATCCCTGATCCCTGATTTGATAGACAT 496
DB 535 CTGTGCTGCACTGTGTACTGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 594
QY 497 AACATGTACATATGACCTCCCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 556
DB 595 TGTCTCTAGAGATGACATCTCTCCCGGTGTGGAAGTCCAGGGGTGACCACTTCTGTGT 654
QY 557 GAGATCCCACTTGTCTGTAAGTTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 615
DB 655 GAGATGCTGTCTTATGTGCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 714
QY 616 ATAGCTGACAGGTGTGACCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 675
DB 715 CTGTGCTGTGGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 773
QY 676 ACTAGTCTTATTCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 735
DB 774 CGTATGTGACAGCGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 833
QY 736 CACCTGTCTTCTTCCACTGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 795
DB 834 CACCTGTCTTCTTCCACTGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 893
QY 796 TGTCTTGGCCAGTTCTTCCAGGCCCCCAACAACAACATCATCTGTGTGTGTGTGTGT 855
DB 894 CCGTGAAGCGGCGCAACAGCTACTTCCAGATATGAGGAAAGTTCTGTGTGTGTGTGTGT 953
QY 856 AATTGTCACTCCAGCCCTGATATCACTCATCTACAGCTTGAAGAAATTAAGAGGTATGCG 915
DB 954 CATGTCTATTTCCACATCAACCCCTCATCTACACTTTGAGGAACAAGATGTGAAGGG 1013
QY 916 GGCCTTGAAGAGGTCTGTGG 936
DB 1014 GACCATGAAGAAACTTGTGG 1034

```

RESULT 5
US-09-524-730-3
Sequence 3, Application US/09524730
Patent No. 6638733

GENERAL INFORMATION:
APPLICANT: Powers, Scott
APPLICANT: Yang, Jianxin
APPLICANT: Cutler, Gene
APPLICANT: Tularik Inc.
TITLE OF INVENTION: No. 6638733el G-Protein Coupled Receptors
FILE REFERENCE: 018781-004710US
CURRENT APPLICATION NUMBER: US/09/524,730
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 3
LENGTH: 1411
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (118)..(1113)
OTHER INFORMATION: human breast cancer amplified G-protein coupled

OTHER INFORMATION: receptor 2 (BCA-GPCR-2)
US-09-524-730-3

Query Match 24.7%; Score 241; DB 4; Length 1411;
Best Local Similarity 55.3%; Pred. No. 8.9e-65;
Matches 509; Conservative 0; Mismatches 410; Indels 2; Gaps 2;

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QY 17 ATCATGAGCTCCGGAATCCACCTTGGGAAGCGGCTTCATCTTGTGGGATTTCTGAT 76
DB 115 ATTATGGAAAGAACATAGCCAGTTACTCAAGGATCATCTGTGGCTTCTGTAT 174
QY 77 GACAGTGGTCTCTGAACTCTCTATGCTAATTTACATCTTATATCTTATGTTGGACTG 136
DB 175 CGGCTGGACTGAGAAATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 234
QY 137 ACCAGGAATGCTGTGCTCTCTGCGCCATCAACATAGAAAGCGGCTCCATGCGCATG 196
DB 235 GTGGCAACACTGCGCATATCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 294
QY 197 TACCTCTGTGGGCAAGCTCTCTCATGAGACCTCTGTTCACATCTGTGTCACTCC 256
DB 295 TACTTCTTCTTGGGAATCTGTCTTTTATGATCTGTCTTTACAGCAAGATTTGCCCT 354
QY 257 AAGCCTTGGGACTTTCGCGAGAGAAAACATATCTCTCTTTGAGGCTGTGCACTT 316
DB 355 CAGCTGTGTGAACTTGGGGGCTTCAGAGAAACATACCTACACAGGCTGTGTGGCC 414
QY 317 CAGATGTTCTGTGCACTGACATAGGATAGCGCTGAGGACCTCTTACTGAGCTTCATGGCC 376
DB 415 CAACCTTACATCTACATATGATGTGGCTTCACAGAGTGTGTGTGTGTGTGTGTGTGTGTGT 474
QY 377 TATGACAGATATGTGGCCATTTGTATCTCTGAAATATCATGACCTTATGAGCCCAAGA 436
DB 475 CATGACCGCTATGTGGCGGTCTGTGCGGTCTGTGACATATGCAAGTATGCGCCACAT 534
QY 437 GTGTGTGATATGTGTGGCCACATCTGTGATCTGTGATCTGTGATCTGTATGAGACAT 496
DB 535 CTGTGCTGTGAGCTGTGTACTGTGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 594
QY 497 AACATGTACATATGACCTCCCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 556
DB 595 TGTCTCTAGAGATGACATCTCTCCCGGTGTGGAAGTCCAGGGGTGACCACTTCTGTGT 654
QY 557 GAGATCCCACTTGTCTGTAAGTTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 615
DB 655 GAGATGCTGTCTTATGTGCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 714
QY 616 ATAGCTGACAGGTGTGACCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 675
DB 715 CTGTGCTGTGGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 773
QY 676 ACTAGTCTTATTCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 735
DB 774 CGTATGTGACAGCGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 833
QY 736 CACCTGTCTTCTTCCACTGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 795
DB 834 CACCTGTCTTCTTCCACTGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 893
QY 796 TGTCTTGGCCAGTTCTTCCAGGCCCCCAACAACAACATCATCTGTGTGTGTGTGTGT 855
DB 894 CCGTGAAGCGGCGCAACAGCTACTTCCAGATATGAGGAAAGTTCTGTGTGTGTGTGTGT 953
QY 856 AATTGTCACTCCAGCCCTGATATCACTCATCTACAGCTTGAAGAAATTAAGAGGTATGCG 915
DB 954 CATGTCTATTTCCACATCAACCCCTCATCTACACTTTGAGGAACAAGATGTGAAGGG 1013
QY 916 GGCCTTGAAGAGGTCTGTGG 936
DB 1014 GACCATGAAGAAACTTGTGG 1034

```

RESULT 6

```

US-08-748-506-8
; Sequence 8, Application US/08748506
; Patent No. 6159707
; GENERAL INFORMATION:
; APPLICANT: Romnett et al.
; TITLE OF INVENTION: NOVEL SPERM RECEPTORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: US
; ZIP: 60601-6780
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,506
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,751
; FILING DATE: 09-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; REFERENCE/DOCKET NUMBER: 74940
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5600
; TELEFAX: 312-616-5700
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 966 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-748-506-8

Query Match      24.3%; Score 237.4; DB 3; Length 966;
Best Local Similarity 55.2%; Pred. No. 9.5e-64;
Matches 463; Conservative 0; Mismatches 376; Indels 0; Gaps 0;

QY 117 TCCTAATCATGTGGCACTGACCAAGCATGCTGCTGCTGCGCATCACCATAAG 176
DB 116 TCATGTTCTTAGTACACTAACAGAAATGCTTCATAGCCCTTGCTATTGTACAGTC 175
QY 177 CCGGCTTCACATGCCCATGTACCTCTGCTGGGAGCTCTCTCTCATGTAGACCTCTGT 236
DB 176 CATCTCTACACACCCCATGTACTTCTTCTGGCCAACTGTCTCTCTGAGATTGGCT 235
QY 237 TCACATCTGTGTGACTGCCAAGGCTTGGGGAGCTTCTGCGCAGAGAAACACTATCT 296
DB 236 ATACTCTGCTGTGATACCAAGATGCTGCAAGCTCTTGAGAGAGGCCGAGAGATCT 295
QY 297 CTTTGGAGGCTGTGACCTTCAGATGTTCTGTGCACTGACATGAGGTAGCGCTAGAGCC 356
DB 296 TTGAGGTGGATGTGGCACAAGATGTTTTCTTCATATTTCTTGATTAATAGAGCT 355
QY 357 TCTACTGGCTTCTATGAGCTTATGACAGATATGTGGCCATTGTTCATCTCTGAATACA 416
DB 356 GCTTATTGGCAGCATGGCTTTGACCGCTATATGCTATATGTTCCCACTCCACTATG 415
QY 417 TGACCTCATGAGGCAAGAGTCTGCTGATCATCATGTGGCACAATCCGATATCTGGCAT 476
DB 416 CAACCCGATAGTCTGAGGTATGTGCTCCACTTGGCAATGTTTCAATGGGTGATGGAT 475
QY 477 CCTGATGTCTATAGACATACATGTACACTATGACCTCTTCTGTGTGTCTGGG 536
DB 476 GCATAGTATGCTCTGGGACAGACCAATTTATTTCTCTTGAACCTTCTGTGAGACCTGTG 535

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QY 537 AATCAGGCATCTCTGTGAGATCCACCTTGTGTAAGTTGGCTGTGTGATACT 596
DB 536 AGATGACCACTTCTTGTGATCTTCCACTTGTGGCACTTGGCTGTGTGATACAT 595
QY 597 CCAGTATGAGCTTATATAGCTGACAGGTGACCTTCTCTGTGCTCCCATTTCTG 656
DB 596 CCAATTTGAGGCTGCACTTGTGTGAGTGTCTCTGATATCTAGCCCTTTTTCG 655
QY 657 CCATTGCGCTCTTACACACTAGTCTTATCTAGTGTCTGTATGACCATMAATGAG 716
DB 656 TGATCATTTATTTTATGATGAGATTCGTGTGAGTGTGTATGCTTCACTGAG 715
QY 717 GGAGAAAGAAAGCCCTTGTACCTGCTCTTCCACCTGATTTGTGTGGATGTTCTATG 776
DB 716 GGCGCACAAAGCCCTTCAACTGTCTCTCCCACTACTTGTGTGATCAGACTTTTATG 775
QY 777 GAGTGCACATTCATGATGTCTTGGCCAGTCTTCCACAGCCCAAGACAGACACA 836
DB 776 GCTAGGATCTTATCTTATTTGAGGCTTAACTTACCTCCTCACAGGAATGGACAAAC 835
QY 837 TCATCTGTTTTTACACATTTGTCACTCCAGCCCTGAATCCACTATCTACAGCCCTGA 896
DB 836 TCTTGGCCCTCTTACACAGCAGTGAATCATGTTGAACCTATATCTATAGTTTAA 895
QY 897 GGATTAAGAGGTATGCGGCTTGTGAGAGGCTCTGGAAATACATCTGCTGGCA 955
DB 896 GGAACAAGATGTACAGCAGCACTGAGAAATTTGGCCCTGAAAAAATTCGTCA 954

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US-08-748-506-5
; Sequence 5, Application US/08748506
; Patent No. 6159707
; GENERAL INFORMATION:
; APPLICANT: Romnett et al.
; TITLE OF INVENTION: NOVEL SPERM RECEPTORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: US
; ZIP: 60601-6780
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,506
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,751
; FILING DATE: 09-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; REFERENCE/DOCKET NUMBER: 74940
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5600
; TELEFAX: 312-616-5700
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 966 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-748-506-5

Query Match      24.3%; Score 237; DB 3; Length 966;
Best Local Similarity 55.1%; Pred. No. 1.3e-63;

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Matches 462; Conservative 0; Mismatches 377; Indels 0; Gaps 0;

QY 117 TCCTATATATGTTGGACCTGACAGCAATGCTGTCTGTCCTGGCCATACCAATAGAG 176
 DB 116 TCATGTTCTTATGATCACTACAGAAATACCTGATGCTGCTATTTGTACCACTC 175
 QY 177 CCCGCTCCACATGCGCCATGATGCTCTGCTGGAGCTCTCTCATGACCTCTGT 236
 DB 176 CATCTCTACAGACCCCATGATGCTCTCTGGCCAACTGCTCTCTGGAGATTGGT 235
 QY 237 TCACATCTGTTGCTACTCCCAAGGCTTGGCGAATCTTCTGGCAGAGAAAACATAT 296
 DB 236 ATACTGCTCTGCTCATACCAAGATGCTGACAGGCTTGTGATGAGCGCAAGATCT 295
 QY 297 CTTTGGAGGCTGTGACCTTGCATGATGCTCTGGCACTGACAAATGGGTAGCGTGAAGAC 356
 DB 296 CTGGGAGGATGTGACACAGATGTTTTTTTGGCATTTTTTGGTATTAACATGATGCT 355
 QY 357 TCCTACTGCTTCATGCGCTTATGACAGGATGATGGCCATTTGTCAATCCTTGAAATACA 416
 DB 356 GCTATTTGGCAGCATGCGCTTTGACCGCTGATGGCCATATGCTCCCACTCACTATG 415
 QY 417 TGACCTCATGAGCCCAAGATGCTGTGATGATGATGAGCCCAATCTTGGATCTGGCAT 476
 DB 416 CAACCCGATGATGAGNGAGTATGCGCCATTTGGCAATTTGATCAATGGGAAATGGGAT 475
 QY 477 CCTGATTTGCTTATGAGCATATACATGATGATGACCTCCCTTCTGTGTCTCTGGAG 536
 DB 476 GATATGATGATGATGAGCAACCAATTTATTTCTCTTGAATCTTGTGACCTCTGG 535
 QY 537 AATGAGGATGCTGCTGTGAGATGCCACCTTGTGAGATGGCTGTGATGATCT 596
 DB 536 AATATGACCATTTCTGTGACCTTCCACTCTCTGACATCTGCTGTGAGATGATCAT 595
 QY 597 CCAAGTATGATGCTTATATATACGTGACAGGTGTGACTTCTCTGCTCTCCCATTTCTG 656
 DB 596 CCAAAACAGAGGCTGACATCTTGTGTGAGTACCTCTGCAATCTTACCCCAATTTTGC 655
 QY 657 CCATTTGGCTCTCTACACATGATGCTTATGATGATGCTGTGATGAGCAATTAAGAG 716
 DB 656 TGATATTTATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 715
 QY 717 GAG 776
 DB 716 GAG 775
 QY 777 GAGCTGCAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 836
 DB 776 GCTGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 835
 QY 837 TCATCTCTGTTTCTACCAATTTGATGATGATGATGATGATGATGATGATGATGATG 896
 DB 836 TCTTGCCCTCTTCTACAGATGATGATGATGATGATGATGATGATGATGATGATGATG 895
 QY 897 GGAATAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 955
 DB 896 GGAACAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 954

RESULT 8
 US-09-546-986A-7
 ; Sequence 7, Application US/09546986A
 ; Patent No. 6635741
 ; GENERAL INFORMATION:
 ; APPLICANT: Powers, Scott
 ; APPLICANT: Yang, Jianxin
 ; APPLICANT: Cutler, Gene
 ; APPLICANT: Tularek Inc.
 ; TITLE OF INVENTION: No. 6635741el G-Protein Coupled Receptors
 ; FILE REFERENCE: 018781-004720US
 ; CURRENT APPLICATION NUMBER: US/09/546,986A
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 09/524,730

PRIOR FILING DATE: 2000-03-14
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 7
 ; LENGTH: 1065
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (26)..(1030)
 ; OTHER INFORMATION: human breast cancer amplified G-protein coupled
 ; OTHER INFORMATION: receptor 4 (BCA-GPCR-4)
 US-09-546-986A-7

Query Match 23.8%; Score 232.4; DB 4; Length 1065;
 Best Local Similarity 53.8%; Pred. No. 3,66-62;
 Matches 479; Conservative 0; Mismatches 411; Indels 0; Gaps 0;

QY 50 GGCTTCATCTTGGTGGGGAATCTGAATGACAGTGGGTCTCTGAACCTGCTATGCTACA 109
 DB 116 GGTTTCATCTTTTGGGTTTCTGATATGCTGATTAAGAGATGCTATTTGTGCTC 175
 QY 110 TTTCATATCTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 169
 DB 176 ATATGATTTCTGATTTTCTATATATTTTGGGAAATACCATATTTCTGTTCTGT 235
 QY 170 ATGAG 229
 DB 236 CTGGAACCAAGCTTCATATGAGCCATGATTTCTCTTCTTCTATCTCTCTCTGATC 295
 QY 230 CTCTGTTACATCTGTTGTGACCTCCCAAGGCTTGGCGGACTTTCTGCGCAGAGAAAC 289
 DB 236 CGCTGCTTACAGCAGAGATGATTTCCCAAGCTCTGATTAACCTGAGGAAACCATGAAA 355
 QY 290 ACTATCTCTTTGAGAGCTGTGACATTCAGATGTTCTGAGCACTGATGATGATGATG 349
 DB 356 ACTATGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 415
 QY 350 GAG 409
 DB 416 GAGTGGCTCTCCGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 475
 QY 410 AATATAG 469
 DB 476 CATTAACATGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 535
 QY 470 CTGAGATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 529
 DB 536 AGTGAATAGCCACACACCTGTGATGATGATGATGATGATGATGATGATGATGATGATG 595
 QY 530 TCTGGGAAATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 589
 DB 596 CATGCGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 655
 QY 590 GATACCTTCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 649
 DB 656 GGCACACAGTTTAAAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATG 715
 QY 650 ATTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 709
 DB 716 GTCTATTTATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 775
 QY 710 AATGAGGAG 769
 DB 776 GCTACCGGAG 835
 QY 770 TTCTATGAGCTGCAATTCATGATGATGATGATGATGATGATGATGATGATGATGATG 829
 DB 836 TTATGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 895
 QY 830 GACACATATCTGTTTCTTACCAATGATGATGATGATGATGATGATGATGATGATGATG 889
 DB 896 GGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 955

QY 890 AGCCGAGGAATAAGAGGATGATGCGGCTTTGAGAGGCTCTGGAAA 939
DB 956 ACCTTGAGATCAAGAGAGTGAAGAGGCAATTAAGAAAGTTTAGCAA 1005

RESULT 9

US-09-524-730-7
Sequence 7, Application US/09524730
Patent No. 6638733
GENERAL INFORMATION:
APPLICANT: Powers, Scott
APPLICANT: Yang, Jianxin
APPLICANT: Cutler, Gene
APPLICANT: Tularik Inc.
TITLE OF INVENTION: No. 6638733el G-Protein Coupled Receptors
FILE REFERENCE: 018781-004710US
CURRENT APPLICATION NUMBER: US/09/524,730
CURRENT FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
LENGTH: 1065
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (26)..(1030)
OTHER INFORMATION: human breast cancer amplified G-protein coupled
OTHER INFORMATION: receptor 4 (BCA-GPCR-4)
US-09-524-730-7

Query Match 23.8%; Score 232.4; DB 4; Length 1065;
Best Local Similarity 53.8%; Pred. No. 3.6e-62;
Matches 479; Conservative 0; Mismatches 411; Indels 0; Gaps 0;

QY 50 GGCTCATCTTGGGGGATTTCTGAATGACAGTGGGTCTCTGACAGCTCTATGCTACA 109
DB 116 GGTTTCACTTTAGGGTCTTCTGATTTAGCTACATTAAGAAAGTTTATTTGTCTC 175
QY 110 TTACATCTCTATCATGTTGGACATGACACGACATGGTCTGCTCTGGCCATCAC 169
DB 176 ATATGATTTCTGATTTACTAATATTTGGGAATACACATCATCTTGTCTCGT 235
QY 170 ATAGAACCCGGCTCCACATGCCATGATCTCTGCTGGGAGCTCTCTCATGAGC 229
DB 236 CTGGAACCCAAAGCTTCAATGCGCATGATTTCTTCTCTCATCTCTCTCTGAC 295
QY 230 CTCTGTTCAATCTGTGTCACTCCCAAGGCTTGGCGCATTTCTGCGGAGAAAAC 289
DB 296 CGCTGCTTACACAGAGTGTATTTCCAGCTCTGTGTAACCTGTGGAAACCATGAAA 355
QY 290 ACTATCTCTTTGAGGCTGTGCACTTCAATGTTCTTGGACATGACATGGGTAGGCT 349
DB 356 ACTATGCGCTATGTTGCTGTGTTGTTGTTCACTTTACAACCTCCATGCCCTGGATCACT 415
QY 350 GAGACCTCTCTACTGGCTTCTGAGGCTTATGACAGGTATGTGGCAATTTGTCATCTCTG 409
DB 416 GAGTGCCTCTCCGGGCTGTGATGCTGTGACCGGTATGTCGTGCGCTCTCTC 475
QY 410 AATATCATGACCTTCATGAGCCCAAGATCTGTGATCATGTGGGCAATCTGTGATC 469
DB 476 CATTAACCTGTTTAAAGCATATCCATCTTGCATGAGCCCTTGGCATTTAGGCAATGCTC 535
QY 470 CTGGCATCTCTGATTTGATAGCATATACATGATACATGACCTCCCTTTCTGTGTG 529
DB 536 AGTGAATAGCAACCACTCTGTGATGATGCACTCCCTCAGCTGCGCTCTTCTGTGGG 595
QY 530 TCTGGGAAATCAGGATCTGTCTGTGAGATCCACCTTGTGAAGTTGGCTGTGCT 589
DB 596 CATGCGCAAGTGAATCTTTCATCTGCGAGGTCCTGTGTCATCAAGCTGGCTTGTGTG 655
QY 590 GATACCTCCAGGTATGAGCTTATTAATATAGTGAAGGTGTGACTTCTCTTGTCTCC 649

DB 656 GGACCAAGTTTACGAGGCTAGCTTTTGTGGCTAGTATCTTTTCTTATATGTGCTT 715
QY 650 ATTTCGCAATTTGGCTCTCTACACATGATCTTATTTCACTGTGCTTGTATGCTATCA 709
DB 716 GTCTCATTCATCCGTGCTCTCTCTGCTACATTTCCACGAGATGTGAGATTAAGTCA 775
QY 710 AATGAGGAGGAAGAAAGCCCTTGTCACTGCTCTTCCACTGATTTGTGTGGATG 769
DB 776 GCTACCCGGAGACGAAGATTTGGGACCTGCTTCTCCACTGACAGTGTGATCACTC 835
QY 770 TTCTATGAGCTGCAATTCATGATGTCTTGGCCAGTTCTCTCCACAGCCCAAGAA 829
DB 836 TTTATGAAACCATCATCTTATGATGTATCTGCAAGCCCAAGATGATGATGAGGACAG 895
QY 830 GACAACATCATCTCTGTTTCTTACACATTTGTCACTGCTCAGCCCTGAAATCCACTATCTAC 889
DB 896 GGCAAGTTGTTTCTCTCTTCTTACATGCTGTGTAACCCGCAATCTTAACCTCTTATTTAT 955

QY 890 AGCCTGAGGAATAAGAGTCAATGCGGCTTGAAGAGGCTCTGGAAA 939
DB 956 ACCTTGAGATCAAGAGGTGAAGAGGCAATTAAGAAAGTTTAGCAA 1005

RESULT 10

US-09-016-434-1115
Sequence 1115, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM.
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 1115:
SEQUENCE CHARACTERISTICS:
LENGTH: 952 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g1336042
US-09-016-434-1115

Query Match 23.6%; Score 230.4; DB 4; Length 952;

Best Local Similarity 54.7%; Pred. No. 1.4e-61;
Matches 499; Conservative 0; Mismatches 411; Indels 2; Gaps 22

[illegible]

```

1  APPLICANT: Powers, Scott
2  APPLICANT: Yang, Jianxin
3  APPLICANT: Cutler, Gene
4  APPLICANT: Tularik Inc.
5  TITLE OF INVENTION: No. 6635741e1 G-Protein Coupled Receptors
6  FILE REFERENCE: 018781-004720US
7  CURRENT APPLICATION NUMBER: US/09/546,986A
8  CURRENT FILING DATE: 2002-04-30
9  PRIOR APPLICATION NUMBER: US 09/524,730
10 PRIOR FILING DATE: 2000-03-14
11 NUMBER OF SEQ ID NOS: 16
12 SOFTWARE: PatentIn Ver. 2.1
13 SEQ ID NO 1
14 LENGTH: 1035
15 TYPE: DNA
16 ORGANISM: Homo sapiens
17 FEATURE:
18 NAME/KEY: CDS
19 LOCATION: (42)..(974)
20 OTHER INFORMATION: human breast cancer amplified G-protein coupled
21 receptor 1 (BCA-GPCR-1)
22 US-09-546-986A-1

```

Query Match	23.4%;	Score 228.4;	DB 4;	Length 1035;
Best Local Similarity	55.0%;	Pred. No. 6.2e-61;		
Matches 448;	Conservative 0;	Mismatches 366;	Indels 0;	Gaps 0;

Qy	122	TACATGTTGGCAGCTGACAGCAAGATGCTGCTGCTCGGCACTACCAATAGAAAGCCGG	181
Db	135	TATGTCGTGGCCATGTTGGGAACTGCCCATCATCTGGAGATCCGGGTGATCTCGAA	194
Qy	182	CTCCACATGCCATGTATACCTCCGTGTTGGGAGCTCTCTCATAGSACCTCTGTTACA	241
Db	195	CTCCAGAGCCCATGTATACCTCTCTCATGTATACCTGTCTCTCGAGACCTCTGTACACC	254
Qy	242	TCTGTTGTCACTCCCAAGGCTTTGGCGGACTTTCTGGCAGAGAAAACATACTCTTT	301
Db	255	ACCAGACAGTCCCTCAGATGTGGTCAACATGGGAGATTTCCGAAAGACCATCAGTAT	314
Qy	302	GGAGGCTGTGCACCTCAGATGTTCCGTGGCACTGACATAGGGGTACGGCTGAGACCTCTA	351
Db	315	GGAGGCTGCACTGTGCATATGCACTCTTCCACTGCTGGGATGACAGAGTGCATGTC	374
Qy	362	CTAGCCTTCATGGCCTATGACAGATATGAGCCATTTGTCACTCTCGAAATACATAGCC	421
Db	375	CTGGCCGCATAGCCCTGTGAACCGCTACCTGGCCAGCTGCAGAGCCCTGCATAGCCGTT	434
Qy	422	CTCAGAGCCCAAGAGTGTCTGATCATGCTGGCCACATCTTGATCTTGGCATCTCTG	481
Db	435	CTCATGACCGGTCCTCTCTGACAGAGCTCGTGGCTCGGCTGGCTCAGTGGCTTGCGC	494
Qy	482	ATTGCTATAGCAATPACATATGACATATGACATATGACATCCCTTTCTGTGTGTCTGGAAATC	541
Db	495	AACCTCTTGTGTGAGGTGTCTCTGACGGTGAATGGCAATCTGTGCGGCGGCAAGTCTG	554
Qy	542	AGGCATCTGCTCTGTGAGATCCCAACCTTGTCTGAAGTTGGCTGTGCTGATACCTCCAGG	601
Db	555	AACAACTTTTCTGTGAGGTGTGCGGCCCTGATCAAGAGTGTGTGTGCGACACCGTATG	614
Qy	602	TATGAGCTTAAATATACGTGACAGGTGACATTTCTTGTCTCCCATTTCTTGCAATT	661
Db	615	AATGACACCAATCTGGCTGTGGTGGCTCTTCTCTGTGTGGTGGCCCTGGGCTCTATC	674
Qy	662	GTTGGCTCTTCAACACACTATCTCTATTACTGTGCTGTGTATGSCATCAAAATGAGGGGAGG	721
Db	675	CTTCTCTCTTAATGCTTATATGCCCCGGGAGTGTCAAGATCAAGTCTCTCAAGGAGACA	734
Qy	722	AAGAAAGCCTTGTCACTGCTCTTCCCACTGATTTGTGTGGGATGTTCTATAGAGCT	781
Db	735	CACAAAGCCTTTGGAGCGATTTCTCTCCACCGATGATGTCTCCCTTCTTACCTACCT	794
Qy	782	GCCAACTCAATGATGTTCTTGGCCAGTTCTTTCACAGAGCCCAAAACAGACATATATC	841

Db 795 GCGATTACATGATCTGAGCCCTTCAGCTACTCCCAAGAGGGAATTAT 854
QY 842 TCTGTTTCTACAAATGTCATCTCGACCTGAAATCCATCATTAAGCCTGAGAA 901
Db 855 TCTCTCTTCTATTCATATATCAACCCCACTCTCAATCCCTTACCTAGACCTGAGAA 914
QY 902 AAGAGGTCATGCGGCGCTTGAAGAGGAGGCTCTGG 935
Db 915 AAAGATATGAAGGGGCTCTGAGAGGACTTCTGG 948

RESULT 12

US-09-524-730-1
Sequence 1, Application US/09524730
Patent No. 6638733
GENERAL INFORMATION:
APPLICANT: Powers, Scott
APPLICANT: Yang, Jianxin
APPLICANT: Cutler, Gene
APPLICANT: Tularik Inc.
TITLE OF INVENTION: No. 6638733el G-protein Coupled Receptors
FILE REFERENCE: 018781-004710US
CURRENT APPLICATION NUMBER: US/09/524,730
CURRENT FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 1
LENGTH: 1035
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (42)..(974)
OTHER INFORMATION: human breast cancer amplified G-protein coupled
US-09-524-730-1

Query Match 23.4%; Score 228.4; DB 4; Length 1035;
Best Local Similarity 55.0%; Pred. No. 6.2e-61;
Matches 448; Conservative 0; Mismatches 366; Indels 0; Gaps 0;

QY 122 TACATGTTGGCACTGACCAAGATGTCGTGCTCTGGCGCATCAGCATAGAACCCGG 181
Db 135 TATGTGCTGGCCATGTTGGGGAAGTCGCCATCATCTGGATGCCGGGTGATCTCAA 194
QY 182 CTCACATGCCCAGTATGCTCTGCTGGAGGCTCTCTCTCATGAGACCTCTGTTACA 241
Db 195 CTCACAGCCCCAGTATGCTCTGCTGACCTGCTCTCTGAGACCTCTGTTACACC 254
QY 242 TCTGTTGCTACTCCCAAGGCTTGGCGGACTTCTGCGCAGAGAAAACATATCTCTT 301
Db 255 AACACGACAGTCTCCAGATGCTGTCACATGAGGAGTTCAGAGAACATAGATAT 314
QY 302 GAGGCTGTCACCTTGATGTTCTGCGCATGACATAGAGTGGCTGAGACCTCTCA 361
Db 315 GAGGCTGTCACCTTGATGTTCTGCGCATGACATAGAGTGGCTGAGACCTCTCA 374
QY 362 CTGGCTTCATGCGCTATGACAGGTATGTCGCAATTTGTCATCTGAATACATGACC 421
Db 375 CTGGCGGCGCATGCGCTGAGACCGCTAGTGGCCAGCTGAGACCGCTGATGCCGT 434
QY 422 CTGATGAGCCCAAGAGTCTGCTGATCATGTCGCGCACATCTGATCTGGCATCTCTG 481
Db 435 CTGATGAGCCCGTCTGTCGTCAGACAGCTGTCGCTGCTGAGCTGAGCTTGGC 494
QY 482 ATTGCTATAGACATACATGATACATGACATCTGCTCTGTCGTGCTCTGGAAATC 541
Db 495 AATCTCTGTCGAGAGTGTCTGAGAGGTCGATGAGATTTGCAATTTGCGCGGCGAGGCTG 554
QY 542 AGGCACTCTGCTGTCGATGATCCACCTTGTGTAAGTTGGCTGTGTCATCTTCAGG 601
Db 555 AACCACTTTTCTGTAGAGTGTGCGGCGGTGATCAAGCTGTGTCGTGTCAGACCGCTAG 614

QY 602 TATGACTTATATATACGTGACAGGTGTGACTTTCCTCTGCTCCCATTTTCGCATT 661
Db 615 AATGACACCAATACCTGGCTGTGCTGTGAGCCCTTCTTGCTGTGAGCCCTGCTCATC 674
QY 662 GTGACCTTCACACATAGTCCATATCATCTGTGCTTGTATGCCATCAATAGAGGGAG 721
Db 675 CTCTCTCTATGAGCTTATATGCCCCGAGCTGTGACAGATTCAGTCTCCCAAGGAGGA 734
QY 722 AAGAAAGCCCTTGTACCTGCTCTTCCCACTGATGTCGAGGATGTTCTATGAGACT 781
Db 735 CACAAGGCTTTGGAGAGTGTCTCTCCCACTGATGATGTCCTCCCTCTTACCTACT 794
QY 782 GCGACATTCATGATGTCCTGCGCAGTTCCTTCACAGCCCAACAAACACATCATC 841
Db 795 GCGATTACATGATCTGACAGCCCTTCCAGCTACTCCCAAGAGGCGCAATTAT 854
QY 842 TCTGTTTCTACAAATTTGTCATCTCGACCTGTAATCATCATCTAGAGCTGAGAA 901
Db 855 TCTCTCTTATTCATATATCAACCCCACTCTCAATCCCTTACCTACACCTTGAGAA 914
QY 902 AAGAGGTCATGCGGCGCTTGAAGAGGAGTCTCTGG 935
Db 915 AAAGATATGAAGGGGCTCTGAGAGGACTTCTGG 948

RESULT 13

US-08-748-506-6
Sequence 6, Application US/08748506
Patent No. 6159707
GENERAL INFORMATION:
APPLICANT: Ronnett et al.
TITLE OF INVENTION: NOVEL SPERM RECEPTORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voie & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: US
ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,506
FILING DATE: 08-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,751
FILING DATE: 09-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION: 74940
REFERENCE/DOCKET NUMBER: 74940
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5600
TELEFAX: 312-616-5700
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 966 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-748-506-6

Query Match 23.2%; Score 226.4; DB 3; Length 966;
Best Local Similarity 54.2%; Pred. No. 2.5e-60;
Matches 455; Conservative 0; Mismatches 384; Indels 0; Gaps 0;

QY 117 TCTATATACATGTTGGACATGACCAAGATGTCGTGCTCTGCGCATCATCATAGAG 176

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Db      116 TCATGTTCTTAGTATCACTAACAAGAAATGCTCTCATAGCCCTGCTGNTTGTACAGATC 175
QY      177 CCGGGCTCCACATGCCCATGTAACCTCTGCTGGAGAGCTCTCTCTCATGAGACCTCCTGT 236
Db      176 CATCTCAACAACCCCATGTAATCTTCTGGGCAACTCTCTCTCTGAGATGGCT 235
QY      237 TCACATCTGTTGACATGCCCAAGGCTTGGGAGCTTCTGCGAGAGAAACACTATCT 296
Db      236 ATACTGCTCTGTATACCAAGATGCTGCAGAGCCTTGTATGAGAGCCAGAAGATCT 295
QY      297 CTTTGGAGGCTGTGCACTTCAATGTTCTGTGCACTGACAAAGGTAAGCGCTGAGAC 356
Db      296 CTAGGAGGAGATGTCACACAGATGTTTCTTCAATTTTGGCAATGAGTGTCT 355
QY      357 TCTTACTGGCTTCAATGCTTATGACAGATGATGAGCCATTTGTATCTCTGAAATCA 416
Db      356 GCTTATGAGCAGCATGAGCTTTTGGCGCTGATGAGGATATGCTCCCATCCCACTATG 415
QY      417 TGACCCCTCATGAGCCCAAGAGCTGCTGATCATGATGAGGCAATCTGGAATCCCTGAGAT 476
Db      416 CAACCCGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 475
QY      477 CCTGATTTGATATAGACATACCATGATGATGATGATGATGATGATGATGATGATGAT 536
Db      476 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 535
QY      537 AAATGAGCATCTGCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 596
Db      536 AGATGAGCATCTCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 595
QY      597 CCAGTATGAGCTTATATATATATATATATATATATATATATATATATATATATATAT 656
Db      596 CCAAAAAGAGGCTCCATCTTGTGAGAGCATCTCTGTATATCTAGTCCATTTTGG 655
QY      657 CCATTTGGGCTCTCAACAACATGATCTATTCATCTGTGCTTGTATGATGATGATGATG 716
Db      656 TGATCTTATATCTTATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 715
QY      717 GAGAGAAAGAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 776
Db      716 GCGGCAATTAAGCTTTTCAACATGATGATGATGATGATGATGATGATGATGATGATGAT 775
QY      777 GAGTGCACATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 836
Db      776 GCTCTGTCTCTTACATCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGT 835
QY      837 TCATCTGTCTTCTTCAACAATGATGATGATGATGATGATGATGATGATGATGATGAT 896
Db      836 TCTTGAGCTCTTCTTCAACAAGATGATGATGATGATGATGATGATGATGATGATGAT 895
QY      897 GGAATTAAGAGTCAATGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGG 955
Db      896 GGAACAAGAGTCAAGGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGG 954

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RESULT 14
US-09-546-986A-5
; Sequence 5, Application US/09546986A
; Patent No. 6635741
; GENERAL INFORMATION:
; APPLICANT: Powers, Scott
; APPLICANT: Yang, Jianxin
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. 6635741e1 G-Protein Coupled Receptors
; FILE REFERENCE: 018781-004720US
; CURRENT APPLICATION NUMBER: US/09/546,986A
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 09/524,730
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5

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; LENGTH: 1351
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (86)..(1108)
; OTHER INFORMATION: human breast cancer amplified G-protein coupled
; OTHER INFORMATION: receptor 3 (BCA-GPCR-3)
US-09-546-986A-5

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Query Match 22.9%; Score 223.6; DB 4; Length 1351;
Best Local Similarity 54.8%; Pred. No. 2.2e-59;
Matches 442; Conservative 0; Mismatches 364; Indels 0; Gaps 0;

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QY      120 TATACATGTTGAGCACTGACCAAGATGATGATGATGATGATGATGATGATGATGATGAT 179
Db      249 TTTACATGATATCATCTTGGGCAATGATGATGATGATGATGATGATGATGATGATGAT 308
QY      180 GAGTCCAGATGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 239
Db      309 ACCTCCACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 368
QY      240 CATCTGTTGATCTCCCAAGGCTTGGGAGCTTGTGCGAGAGAAACATATCTCT 299
Db      369 CCAGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 428
QY      300 TTGAGGCTGTGACCTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 359
Db      429 ATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 488
QY      360 TACTGAGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 419
Db      489 TGCTGGCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 548
QY      420 CCTCATGAGCCCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 479
Db      549 TCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 608
QY      480 TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 539
Db      609 CCACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 668
QY      540 TCAGGATCTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 599
Db      669 TCAGCACTTCTTGTGCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 728
QY      600 GGTATGACTTATATATATATATATATATATATATATATATATATATATATATAT 659
Db      729 TCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 788
QY      660 TTGTGGCTCTCTCAACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 719
Db      789 TCTGTGCTCTTAAAGGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 848
QY      720 GGAAGAAAGCTTGTCACTGCTCTTCCACATGATGATGATGATGATGATGATGATGAT 779
Db      849 GGAAGAAAGCATTAACAACCTGCTCTTCCACAGCTGATGATGATGATGATGATGAT 908
QY      780 CTGGCAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 839
Db      909 GCATATCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 968
QY      840 TCTGTGTTTCTTACAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 899
Db      969 TAGCTCTGTCTTACACCGATGATGATGATGATGATGATGATGATGATGATGATGAT 1028
QY      900 ATAAGAGTCAATGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGG 925
Db      1029 ACACGAGGATGAAGGCGCTCCGG 1054

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RESULT 15
US-09-524-730-5

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PS Claim 8; Page 10; 111pp; English.

CC The present sequence is that of a nucleic acid encoding a novel human G-protein coupled receptor, designated GPCR1, that has structural and physiological functions characteristic of the olfactory receptor family. CC The invention provides GPCR1 polypeptides, nucleic acids and antibodies. CC These are useful for treating or preventing a GPCR1-associated disorder, such as cardiomyopathy, atherosclerosis, diabetes, or a disorder related to cell signal processing or metabolic pathway modulation in humans (claimed). They may further be used for treating or preventing e.g. developmental diseases, metabolic pathway disorders, retinal disorders, wasting disorders associated with chronic diseases, pain, cancer, psychotic and neurological disorders (e.g. anxiety or schizophrenia), autoimmune diseases, allergies, bacterial, fungal, protozoal and viral infections, neurodegenerative diseases (e.g. Alzheimer's disease), and haematopoietic diseases. The proteins and nucleic acids may also be used as research tools, as diagnostic or prognostic markers, in gene therapy, for promoting tissue regeneration in vitro and in vivo, and as biological defence weapons. The nucleic acids may also be used in chromosome mapping, in tissue typing, in forensic biology (e.g. to identify individuals from minute biological samples), in forensic identification of a biological sample, as surrogate markers, and in pharmacogenomics

XX Sequence 977 BP; 215 A; 279 C; 220 G; 263 T; 0 U; 0 Other;

Query Match 100.0%; Score 977; DB 6; Length 977;

Best Local Similarity 100.0%; Pred. No. 4.1e-285; Mismatches 0; Gaps 0;

Matches 977; Conservative 0; Indels 0; Gaps 0;

QY 1 GCACTTAAAAAACAATCATGAGAGCTCCGAGACTCCACTTGGGAAAGCGCTCATCTT 60
DB 1 GCACTTAAAAAACAATCATGAGAGCTCCGAGACTCCACTTGGGAAAGCGCTCATCTT 60
QY 61 GGTGGGAGATTCTGATGACAGTGGGCTCTCTGAACTGCTTAATGCTTAACTTCAATCTT 120
DB 61 GGTGGGAGATTCTGATGACAGTGGGCTCTCTGAACTGCTTAATGCTTAACTTCAATCTT 120
QY 121 ATACATGTTGGCACTGACACCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 121 ATACATGTTGGCACTGACACCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 121 ATACATGTTGGCACTGACACCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 121 ATACATGTTGGCACTGACACCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 181 GCTCCACATGCTCCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 181 GCTCCACATGCTCCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 241 ATCTGTTGCTACTGCCAAGGCTTGGGCGAATTTCTGGCGAGAGAAAACATATCTCTT 300
DB 241 ATCTGTTGCTACTGCCAAGGCTTGGGCGAATTTCTGGCGAGAGAAAACATATCTCTT 300
QY 301 TGGAGGCTGTCACATTCAGATGTTCTTGGCACTGACATGCTGGTGGGAGACCTCT 360
DB 301 TGGAGGCTGTCACATTCAGATGTTCTTGGCACTGACATGCTGGTGGGAGACCTCT 360
QY 301 TGGAGGCTGTCACATTCAGATGTTCTTGGCACTGACATGCTGGTGGGAGACCTCT 360
DB 301 TGGAGGCTGTCACATTCAGATGTTCTTGGCACTGACATGCTGGTGGGAGACCTCT 360
QY 361 ACTGACCTTCAATGAGGCTTGAAGATGATGAGGCTTGAAGATGATGAGGCTTGAAGAT 420
DB 361 ACTGACCTTCAATGAGGCTTGAAGATGATGAGGCTTGAAGATGATGAGGCTTGAAGAT 420
QY 361 ACTGACCTTCAATGAGGCTTGAAGATGATGAGGCTTGAAGATGATGAGGCTTGAAGAT 420
DB 361 ACTGACCTTCAATGAGGCTTGAAGATGATGAGGCTTGAAGATGATGAGGCTTGAAGAT 420
QY 421 CCTCATGAGCCCAAGAGTCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 480
DB 421 CCTCATGAGCCCAAGAGTCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 480
QY 481 GATTGCTTATGAGCACTTACATGATGATGATGATGATGATGATGATGATGATGATGAT 540
DB 481 GATTGCTTATGAGCACTTACATGATGATGATGATGATGATGATGATGATGATGATGAT 540
QY 541 CAGGATCTGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
DB 541 CAGGATCTGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
QY 601 GTATGAGCTTATATATAGTACAGAGTGTGATCTTCTCTCTCTCTCTCTCTCTCTCTCT 660
DB 601 GTATGAGCTTATATATAGTACAGAGTGTGATCTTCTCTCTCTCTCTCTCTCTCTCTCT 660

QY 661 TGTGGCTCCTTACACACTAGTCTTATCTAGTGTGCTTGTATGCAATCAATGAGGAGG 720
DB 661 TGTGGCTCCTTACACACTAGTCTTATCTAGTGTGCTTGTATGCAATCAATGAGGAGG 720
QY 721 GAAAGAAAGCCCTTGTACACTGCTCTTCCACCTGATGTTGGTGGGATGTTCTTATGAGC 780
DB 721 GAAAGAAAGCCCTTGTACACTGCTCTTCCACCTGATGTTGGTGGGATGTTCTTATGAGC 780
QY 781 TGGCACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
DB 781 TGGCACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY 841 CTCTGTTTTCATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
DB 841 CTCTGTTTTCATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
QY 901 TAAAGAGGTCATGCGGCGCTTGAAGAGGCTTGGGAAATATCATATGCTTGGACATTC 960
DB 901 TAAAGAGGTCATGCGGCGCTTGAAGAGGCTTGGGAAATATCATATGCTTGGACATTC 960
QY 961 CAGGCTCTAGGAAAGGA 977
DB 961 CAGGCTCTAGGAAAGGA 977

RESULT 2

AAH31857 standard; DNA; 947 BP.

AAH31857;

30-JUL-2001 (first entry)

Human olfactory receptor polynucleotide, SEQ ID NO: 430.

Human; olfactory receptor; OR; primary scent determination;

secondary scent determination; polypeptide library; odour receptor;

scent profile; scent fingerprint; scent representation; ds.

Homo sapiens.

MO200127158-A2.

19-APR-2001.

06-OCT-2000; 2000MO-US027582.

08-OCT-1999; 99US-0158615P.

24-FEB-2000; 2000US-0184809P.

(DIGI-) DIGISCENTS.

(YEDA) YEDA RES & DEV CO LTD.

Belenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;

WPI; 2001-290713/30.

New polynucleotides which encode polypeptides involved in olfactory

sensation for identifying olfactory agonists and antagonists.

Claim 8; Page 352; 1857bp; English.

The present sequence is one of a number of isolated polynucleotides which encode polypeptides involved in olfactory sensation. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a

CC neuronal tissue, in production of transgenic plants and for the
 CC development of new drug targets for various disorders. This sequence
 CC represents DNA encoding a human OR protein

XX Sequence 1050 BP; 234 A; 293 C; 238 G; 285 T; 0 U; 0 Other;

Query Match 85.5%; Score 835; DB 5; Length 1050;

Best Local Similarity 91.2%; Pred. No. 4,4e-242;

Matches 886; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

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QY 7 AAAAAACACATCATGAGAGCTCCGAACTCCACTTGGGAAAGCGGCTTCATCTTGGTGG 66
DB 59 AAGAAACACAGCATGAGAGCTCTGAACTTCACTTGGGAAAGTGGCTTCAATTTGGTGG 118
QY 67 GATCTGAATGAGAGTGGTCTCTGAACTGCTATGATGATCAATTTCAATCTATACAT 126
DB 119 GATTCTGAATGAGAGTGGTCTCTGAACTGCTCTGAACTGCTATGAACTTCAATCTTACTT 178
QY 127 GTTGGCACTGACAGCATGAGTGTGCTGCTCTGCTGCGACATCAACATAGAAAGCCGGCTCA 186
DB 179 GTTGGCCCTGATGACGATGAGCTTACGCTCTGGCTATGACGATGAAAGCCGGCTCA 238
QY 187 CATGCCCATGATGATCTCTGCTGGGAGCTCTCTCTCATGAGACCTCTGTTCAATCTGT 246
DB 239 CATGCCCATGATGATCTCTGCTGGGAGCTCTCTCTCATGAGACCTCTGTTCAATCTGT 298
QY 247 TGTGACTCCCAAGGCTTGGGGAGCTTCTGCGAGAGAGAAACAATACTCTCTTGGAGG 306
DB 299 TGTGACTCCCAAGGCTTGGGGAGCTTCTGCGAGAGAGAAACAATACTCTCTTGGAGG 358
QY 307 CTGTCGACCTTGAATGTTCTCTGCGACATGACATGGGTAGCCGTGAGAGACCTCTTATGGC 366
DB 359 CTGTCGACCTTGAATGTTCTCTGCGACATGACATGGGTAGCTGTGAGGAGCTCTTATGGC 418
QY 367 CTTCATGAGCCATGACAGATGATGAGGCGATTTGATCTCTGAAATTCATGACCTTCAT 426
DB 419 CTTCATGAGCCATGACAGATGATGAGGCGATTTGATCTCTGAAATTCATGACCTTCAT 478
QY 427 GAGCCCAAGAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 486
DB 479 GAGCCCAAGAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 538
QY 487 TATAGACATATCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 546
DB 539 CCTATATATATACCGGTATATACATGATGATGATGATGATGATGATGATGATGATGATG 598
QY 547 TCTGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 606
DB 599 TCTGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 658
QY 607 GCTTATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 666
DB 659 GCTTATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 718
QY 667 CTCTACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 726
DB 719 CTCTACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 778
QY 727 AGCCCTTGTCACTGCTCTCTCCCACTGATGATGATGATGATGATGATGATGATGATG 786
DB 779 AGCCCTTGTCACTGCTCTCTCCCACTGATGATGATGATGATGATGATGATGATGATG 838
QY 787 ATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 846
DB 839 ATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 898
QY 847 TTTCTACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 906
DB 899 TTTCTACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 958
QY 907 GGTATGAGGGGCTTGGAGAGGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 966
DB 959 GGTATGAGGGGCTTGGAGAGGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1018
  
```

QY 967 CTAGGAGAGA 977
 DB 1019 CTAGGAGAGA 1029

RESULT 4

ADCC85822
 ID ADCC85822 standard; DNA; 1351 BP.

XX ADCC85822;

XX 01-JAN-2004 (first entry)

XX Human GPCR gene SEQ ID NO:275.

XX ds; gene; human; GPCR;

XX guanosine triphosphate-binding protein coupled receptor; gene therapy.

XX Homo sapiens.

XX EPI270724-A2.

XX 02-JAN-2003.

XX 18-JUN-2002; 2002EP-00013517.

XX 18-JUN-2001; 2001JP-00246789.

XX (NAD-) NNT INST ADVANCED IND SCI & TECHNOLOGY.

XX (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

XX Suwa M, Asai K, Akiyama Y, Aburatani H;

XX MPI; 2003-315783/31.

XX P-PSDB; ADCC85823.

XX New polynucleotide, useful for preparing a composition for treating a

XX patient in need of increased or suppressed activity or expression of the

XX guanosine triphosphate-binding protein coupled receptor.

XX Claim 1; SEQ ID NO 275; 28pp; English.

XX The invention relates to a novel polynucleotide encoding a guanosine

XX triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of

XX the invention may have a use in gene therapy. The polynucleotide and

XX polypeptide are useful for preparing a composition for treating a patient

XX in need of increased or suppressed activity or expression of the

XX guanosine triphosphate-binding protein coupled receptor. The

XX polynucleotide sequences shown in ADCC8548-ADCC87616 encode GPCR's of the

XX invention.

XX Sequence 1351 BP; 342 A; 340 C; 295 G; 374 T; 0 U; 0 Other;

XX Query Match 85.5%; Score 835; DB 9; Length 1351;

XX Best Local Similarity 91.2%; Pred. No. 5e-242;

XX Matches 886; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

```

QY 7 AAAAAACACATCATGAGAGCTCCGAACTCCACTTGGGAAAGCGGCTTCATCTTGGTGG 66
DB 188 AAGAAACACAGCATGAGAGAGCTCTGAACTTCACTTGGGAAAGTGGCTTCAATTTGGTGG 247
QY 248 GATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 307
DB 307 GATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 367
QY 367 GATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 427
DB 427 GATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 487
  
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	QY	247	TGTCACTCCCAAGACCTTGGCGGACATTTCGGCGCAGAGAAAAACATATCTCTTTGGAG	306
QY	247	TGTCACTCCCAAGACCTTGGCGGACATTTCGGCGCAGAGAAAAACATATCTCTTTGGAG <td>306</td>	306	
Db	428	TGTCACTCCCAAGACCTTGGCGGACATTTCGGCGCAGAGAAAAACATATCTCTTTGGAG	487	
QY	307	CTGTGACACTCAGATGTTCTCGGCACGTGAAATGGGTAGCGCTGAGGACCTCTTACTGGC	366	
Db	488	CTGTGACCTTCAAGATGTTCTCGGCACGTGAAATGGGTAGCGCTGAGGACCTCTTACTGGC	547	
QY	367	CTTCATGGCCTATGACAGATATGGCCAAATTTGTCACTCTCTGAAATATACAGCCCTAT	426	
Db	548	CTTCATGGCCTATGACAGATATGGCCAAATTTGTCACTCTCTGAAATATACAGCCCTAT	607	
QY	427	GAGCCCAAGAATCTGCTGATATATGGTGGCCCAATCTGGAATCTCGGCATCCCTGATTGC	486	
Db	608	GAGCTCAAGAGCTGCTGCTGATATATGGTGGCCCAATCTGGAATCTCGGCATCCCTGATTGC	667	
QY	487	TATAGACATATACATGATACATATGACCTCCCTTTCTGTGTCTCTGGGAAATCAGGCA	546	
Db	668	CCTAATATATACCGTATATACATGATACATATGACCTCCCTTTCTGTGTCTCTGGGAAATCAGGCA	727	
QY	547	TCTGCTCTGTGATATCCCAACCTTGTGTAAGTTGGCTGTGCTGATACCTCCAGGATATGA	606	
Db	728	TCTGCTCTGTGATATCCCAACCTTGTGTAAGTTGGCTGTGCTGATACCTCCAGGATATGA	787	
QY	607	GCTTATATATATCGTGACAGGTGTGACTTCTCTTGTCTCCCATTTCTGCATATGTGGC	666	
Db	788	GCTCATATGATATGATATGGGTGTGACCTTCTGTGATCCCTCTCTTGTGCTATATCTGGC	847	
QY	667	CTCTACACATACATAGCTATATACATGCTGTGTTGTGATATGCAATGAATGAGGGAGAGAA	726	
Db	848	CTCTATATACAAATTTCTACTACTGTGCTCATATATGCTATGAATGAGGGAGAGAA	907	
QY	727	AGCCCTTGTCACTGCTCTTCCCAACCTGATTTGGTCGAGATGTTCTATGAGCTGGCAC	786	
Db	908	AGCCCTTGTCACTGCTCTTCCCAACCTGATTTGGTCGAGATGTTCTATGAGCTGGCAC	967	
QY	787	ATTATATGATGCTTGGCCCAAGTTCTCTTCCACAGCCCCAAACAGCAACATATCTCTGT	846	
Db	968	ATTATATGATGCTTGGCCCAAGTTCTCTTCCACAGCCCCAAACAGCAACATATCTCTGT	1027	
QY	847	TTTTCACCAATTTGTCACTCCAGCCCTGAATTCATCTCATACAGCTGAGGAATTAAGA	906	
Db	1028	TTTTCACCAATTTGTCACTCCAGCCCTGAATTCATCTCATACAGCTGAGGAATTAAGA	1087	
QY	907	GGTATGCGGGCTTGGAGAGGGTCTCTGGGAAAAATACATATCTGTCGACATTTCCAGCT	966	
Db	1088	GGTATGCGGGCTTGGAGAGGGTCTCTGGGAAAAATACATATCTGTCGACATTTCCAGCT	1147	
QY	967	CTAGGAGAAAGA 977		
Db	1148	CTAGGAGAAAGA 1158		
RESULT 5				
AAS11688				
ID	AAS11688 standard; DNA; 1008 BP.			
XX	AAS11688;			
XX	24-OCT-2001 (first entry)			
DE	Human odorant receptor (OR) DNA #5.			
XX	Human; olfactory receptor; OR; G-protein coupled receptor superfamily;			
KW	GPCR; gene therapy; tranquilizer; vulnery; anti-HIV; cytostatic; ds;			
KW	nootropic; neuroprotective; antiparkinsonian; antialzheimer's; cancer;			
KW	antiinflammatory; odorant receptor; olfactory loss; trauma; HIV;			
KW	human immunodeficiency virus; neoplastic growth; neurological disorder;			
KW	Parkinson's disease; Alzheimer's disease; neurogenesis; Crohn's disease;			
KW	wound healing; asthma; Alzheim hereditary osteodystrophy;			
XX	multiple sclerosis; nasal epithelial neuronal tissue; transgenic plant.			

OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	27..1001
FT		/tag= a
FT		/product= "Human odorant receptor protein #5"
XX		
PN	MO200157215-A2.	
XX		
PD	09-AUG-2001.	
XX		
PF	07-FEB-2001; 2001MO-US003923.	
XX		
PR	07-FEB-2000; 2000US-0180511P.	
PR	07-FEB-2000; 2000US-0180630P.	
PR	07-FEB-2000; 2000US-0180646P.	
PR	08-FEB-2000; 2000US-0180930P.	
PR	08-FEB-2000; 2000US-0181004P.	
PR	08-FEB-2000; 2000US-0181013P.	
PR	08-FEB-2000; 2000US-0181043P.	
PR	24-JUL-2000; 2000US-0220262P.	
PR	25-JUL-2000; 2000US-0220594P.	
PR	11-AUG-2000; 2000US-0224596P.	
PR	02-NOV-2000; 2000US-0245292P.	
PR	06-FEB-2001; 2001US-00777789.	
PA	(CURA-) CURAGEN CORP.	
XX		
PI	Padigar M, Spytek KA, Li L, Ballinger RA, Mishra VS;	
PI	Baumgartner UC;	
XX		
DR	WPI; 2001-488883/53.	
XX		
DR	P-PsDB; AAU07088.	
PT	Novel isolated NOVX polypeptide related to human odorant receptor family	
PT	of G-protein coupled receptor superfamily of proteins useful for treating	
PT	trauma, neoplastic growth, Parkinson's disease, Alzheimer's disease.	
XX		
XX	Claim 9; Page 44; 199P; English.	
XX		
CC	Novel isolated NOVX polynucleotides and their encoded polypeptides of the	
CC	invention are related to the human olfactory (or odort) receptors	
CC	(ORs), from the G-protein coupled receptor (GPCR) superfamily. The	
CC	sequences are useful for treating or preventing a pathology associated	
CC	with OR in a subject, and for manufacturing a medicament for treating a	
CC	syndrome associated with a human disease. These diseases include	
CC	disorders of olfactory loss, such as trauma, HIV illness and neoplastic	
CC	growth, neurological disorders, such as Parkinson's disease and	
CC	Alzheimer's disease, neurogenesis, cancer, wound healing, asthma, Crohn's	
CC	disease, multiple sclerosis, and Albrigth hereditary osteodystrophy. The	
CC	polynucleotides and polypeptides are also useful, to identify proteins of	
CC	the same family, to screen for molecules which inhibit or enhance the	
CC	activity or function of olfactory receptors, to detect nasal epithelial	
CC	neural tissue, in production of transgenic plants and for the	
CC	development of new drug targets for various disorders. This sequence	
CC	represents DNA encoding a human OR protein	
XX		
SQ	Sequence 1008 BP; 216 A; 289 C; 234 G; 269 T; 0 U; 0 Other;	
	Query Match 85.4%; Score 834; DB 5; Length 1008;	
	Best Local Similarity 91.2%; Pred. No. 8.7e-242;	
	Matches 885; Conservative 0; Mismatches 85; Indels 0; Gaps 0;	
OY	8 AAAAAACATCAAGGAGCTCCGGAACTCCACCCTTGGGAACCGCTTATCTTGATGGG 67	
Db	39 AACCAACAGCAGATGAGCTCTGAACTCACCTTGGGAATGGCTCATTTTGGTGGG 98	
OY	68 ATTCTGATGACATGTGGGTCTCTGAACCTGTCATGCTATTACAATCCATACATG 127	
Db	99 ATTCGATGATGACATGTGGGTCTCTGAACCTGTCATGCTATTACAATCCATACATG 158	
OY	128 TTGCACATGACAGCAATGCTTCTGCTCTTGGCCATCAACATAGAAGCCGGCTTAC 187	

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Db      159 TTGGCCCTGATGCAATGGGCTACTGCTCTGCTATATCAACGAGAGCCGGCTCCAC 218
QY      188 ATGCCCATGACTCTCTGCTGGGAGCTCTCTCTATGAGACCTCTGTTCAATCTGTT 247
Db      219 ATGCCCATGACTCTCTGCTGGGAGCTCTCTCTATGAGACCTCTGTTCAATCTGTT 278
QY      248 GTCACCTCCCAAGGCTTGGGAGCTTCTGCGAGAGAAAACATCTCTCTTGGAGGC 307
Db      279 GTCACCTCCCAAGGCTTGGGAGCTTCTGCGAGAGAAAACATCTCTCTTGGAGGC 338
QY      308 TGTGACCTTCAAGTGTCTGCGACATGACATAGGAGTGGCTGAGACCTCTCTA 367
Db      339 TGTGACCTTCAAGTGTCTGCGACATGAGAGTGGCTGAGACCTCTCTA 398
QY      368 TTGATGCTTATGACAGATATGAGGACATTTGTCATCTCTGAAATCATGACCTCATG 427
Db      399 TTGATGCTTATGACAGATATGAGGACATTTGTCATCTCTGAAATCATGACCTCATG 458
QY      428 AGCCCAAGAGCTGCTGGATCATGATGAGGACATCTGATCTGATCTGATCTGAT 487
Db      459 AGCTCAAGAGCTGCTGGATCATGATGAGGACATCTGATCTGATCTGATCTGAT 518
QY      488 ATAGACATACCATGATACATGACATCTCTCTCTGCTGCTGCTGCTGCTGCT 547
Db      519 CTATATATATACCGTATACATGACATCTCTCTCTGAGGCTGAGGATCAGGAT 578
QY      548 CTGCTCTGATGATCTCCACCTTGTCTGATGAGGCTGCTGATCTCTGATGATGAG 607
Db      579 CTCTCTGATGATCTCCACCTTGTCTGATGAGGCTGCTGATCTCTGATGATGAG 638
QY      608 CTATATATATACCGTATACATGACATCTCTCTCTGCTGCTGCTGCTGCTGCT 667
Db      639 CTATATATATACCGTATACATGACATCTCTCTCTGAGGCTGAGGATCAGGAT 698
QY      668 TCTACACACTAGTCTTATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 727
Db      699 TCTATATACAAATTTACTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 758
QY      728 GCGCTTGTACCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 787
Db      759 GCGCTTGTACCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 818
QY      788 TTCAATGATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 847
Db      819 TTCAATGATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 878
QY      848 TTCAACAAATTTACTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 907
Db      879 TTCAACAAATTTACTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 938
QY      908 GTGATGCGGCTTGAAGAGGCTCTGAGAAATATCATAGCTGCGACATTTCCAGGCTC 967
Db      939 GTGATGCGGCTTGAAGAGGCTCTGAGAAATATCATAGCTGCGACATTTCCAGGCTC 998
QY      968 TAGGGAAGGA 977
Db      999 TAGGGAAGGA 1008

```

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RESULT 6
ABK53096
ID ABK53096 standard; cDNA; 1008 BP.
XX ABK53096;
AC
XX
XX 15-AUG-2002 (first entry)
DE
XX cDNA sequence encoding novel odourant receptor NOV6 protein.
XX
XX NOV; odourant receptor; G protein coupled receptor; GPCR; trauma; HIV;
KM 88; gene; olfactory receptor; olfactory loss; neoplastic growth;
KM human immunodeficiency virus; Alzheimer's disease; neurological disorder;
KM Parkinson's disease.

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XX OS Unidentified.
XX XX Location/Qualifiers
XX FH Key 27.1001
XX FT CDS /tag= a
XX FT /product= "NOV6 protein"
XX
XX MO200236632-A2.
XX
XX
XX PD 10-MAY-2002.
XX PE
XX PF 09-OCT-2001; 2001MO-US031744.
XX PR 02-NOV-2000; 2000US-0245292P.
XX PR 06-FEB-2001; 2001US-00777789.
XX PR 20-SEP-2001; 2001US-00245292.
XX
XX PA (CURA-) CURAGEN CORP.
XX
XX PI Alsobrook JP, Burgess CE, Groesse WM, Lepley DW, Padigaru M,
XX PI Spletter KA;
XX
XX DR WPI; 2002-471499/50.
XX DR P-PSDB; AAU97927.
XX
XX PT New isolated olfactory receptor-like polypeptide, NOVX, useful for
XX PT diagnosing, preventing or treating disorders of olfactory loss, e.g.
XX PT trauma, human immunodeficiency virus illness, neoplastic growth and
XX PT neurological disorders.
XX
XX PS Claim 9; Page 33; 122pp; English.
XX
XX CC This invention relates to the DNA and protein sequences of a novel
XX CC isolated olfactory receptor-like polypeptide, NOVX. The DNA and protein
XX CC sequences of the invention and an antibody specific for the protein are
XX CC useful for treating or preventing a disorder associated with NOV1 in a
XX CC subject, preferably human. A NOVX specific antibody is useful for
XX CC determining the presence or amount of protein in a sample. The DNA,
XX CC protein and antibody of the invention is useful for diagnosing,
XX CC preventing or treating disorders associated with aberrant NOVX expression
XX CC such as disorders of olfactory loss, e.g. trauma, human immunodeficiency
XX CC virus (HIV) illness, neoplastic growth and neurological disorders, e.g.
XX CC Parkinson's disease and Alzheimer's disease. The sequences and NOV
XX CC antibody is useful in screening assays, detection assays (e.g.,
XX CC chromosomal mapping, tissue typing, forensic biology), predictive
XX CC medicine (e.g., diagnostic assays, prognostic assays, monitoring clinical
XX CC trials and pharmacogenomic), and in methods of treatment (e.g.,
XX CC therapeutic and prophylactic). The NOV protein is useful as immunogen to
XX CC produce antibodies immunospecific for the protein, to screen for
XX CC potential agonist and antagonist compounds, and as bait protein in a two-
XX CC hybrid or three-hybrid assay. The nucleotide sequence is useful in gene
XX CC therapy, to express the protein, to detect NOVX mRNA or a genetic lesion
XX CC in a NOVX gene, and to modulate NOVX activity. The antibody of the
XX CC invention is useful for isolating, and purifying the protein and to
XX CC monitor protein levels in tissue as part of a clinical testing procedure.
XX CC The present sequence represents the cDNA encoding the NOV6 protein of the
XX CC invention.
XX
XX SQ Sequence 1008 BP; 216 A; 289 C; 234 G; 269 T; 0 U; 0 Other;

```

```

Query Match 85.4%; Score 834; DB 6; Length 1008;
Best Local Similarity 91.2%; Pred. No. 8.7e-242;
Matches 885; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

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```

QY 8 AAAAAACATCATGAGGCTCGGAACCTCCACTTGGGAAAGGCGCTCATCTTGGTGGG 67
Db 39 AACTACCAAGCATGAGCTCTGGAACCTTCACTTGGGAAAGGCGCTCATCTTGGTGGG 98
QY 68 ATTCTGATGACAGTGGGTCTCTGACTGCTTATGCTACATTTAATCTATACATG 127
Db 99 ATTCTGATGACAGTGGGTCTCTGACTGCTTATGCTACATTTAATCTATACATG 158

```

QY 128 TTGGCACTGACCAAGATGATCTGCTGCTCCCTGGCCATCACATAGAGCCCGGCTCCAC 187
 Db 159 TTGGCCCTGATCAGAAATAGGCTCTGCTCTGCTGCTATACAGAGGCGGCTCCAC 218
 QY 188 ATGCCCATGATACCTTCCTGCTGGCAAGCTCTCTCATGAGACTCTGTTCACTGTT 247
 Db 219 ATGCCCATGATACCTTCCTGCTGGCAAGCTCTCTCATGAGACTCTGTTCACTGTT 278
 QY 248 GTCACTCCCAAGGCGCTGGCGGACTTTTGTGGCAGAGAAAACACTATCTCTTTGAGGC 307
 Db 279 GTCACTCCCAAGGCGCTGGCGGACTTTTGTGGCAGAGAAAACACTATCTCTTTGAGGC 338
 QY 308 TGTGCACTTCAGATGTTCTGCTGGCACTGCAATAGGAGTACCGTGAAGACTCTCTGACC 367
 Db 339 TGTGCTCTTGAATGTTCTGCTGGCACTGCAATAGGAGTACCGTGAAGACTCTCTGACC 398
 QY 368 TTCAATGCTTATGACAGGATATGGGCAATTTGATCTCTGAAATACATGACCTCATG 427
 Db 399 TTCAATGCTTATGACAGGATATGGGCAATTTGATCTCTGAAATACATGACCTCATG 458
 QY 428 AGCCCAAGCTCTGCTGATATGATGAGCCCACTGCTGATCTGAGATCTGAGATCTGATTTGCT 487
 Db 459 AGCCCAAGCTCTGCTGATATGATGAGCCCACTGCTGATCTGAGATCTGAGATCTGATTTGCT 518
 QY 488 ATAGGACATACCAATGATACATGATGACCTGCTCTGATGCTGGGAAATCAGGCAT 547
 Db 519 CTATATATATACCGTATATACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 578
 QY 548 CTGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 607
 Db 579 CTGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 638
 QY 608 CTATATATATACCGTATATACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 667
 Db 639 CTATATATATACCGTATATACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 698
 QY 668 TCCATACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 727
 Db 699 TCCATATACCAATTTCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 758
 QY 728 GCCCTTGTGACCTGCTCTTCCACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 787
 Db 759 GCCCTTGTGACCTGCTCTTCCACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 818
 QY 788 TTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 847
 Db 819 TTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 878
 QY 848 TTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 907
 Db 879 TTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 938
 QY 908 GTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 967
 Db 939 GTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 998
 QY 968 TAGGGAAGA 977
 Db 999 TAGGGAAGA 1008

RESULT 7
 AAK53097
 ID AAK53097 standard; cDNA; 1008 BP.
 XX
 AC AAK53097;
 XX
 DT 15-AUG-2002 (first entry)
 XX
 DE cDNA sequence encoding novel odourant receptor NOV7 protein.
 XX
 KW NOV; odourant receptor; G protein coupled receptor; GPCR; trauma; HIV;
 KW ss; gene; olfactory receptor; olfactory loss; neoplastic growth;

KM human immunodeficiency virus; Alzheimer's disease; SNP;
 KW neurological disorder; Parkinson's disease.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT 27..1001
 FT /tag= a
 FT /product= "NOV7 protein"
 FT replace(278,T)
 FT /**tag= b
 FT /standard_name= "Single nucleotide polymorphism"
 XX
 FN W0200236632-A2.
 XX
 PD 10-MAY-2002.
 XX
 PP 09-OCT-2001; 2001WO-US031744.
 XX
 PR 02-NOV-2000; 2000US-0245292P.
 PR 06-FEB-2001; 2001US-00777789.
 PR 20-SEP-2001; 2001US-00245292.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Aisobrook JP, Burgess CE, Grosse WM, Lepley DM, Padigaru M;
 PI Spytek KA;
 XX
 DR WPI: 2002-471499/50.
 DR P-PSDB; AAU97928.
 XX
 PT New isolated olfactory receptor-like polypeptide, NOVX, useful for
 PT diagnosing, preventing or treating disorders of olfactory loss, e.g.
 PT trauma, human immunodeficiency virus illness, neoplastic growth and
 PT neurological disorders.
 XX
 PS Claim 9; Page 34; 122pp; English.
 XX
 CC This invention relates to the DNA and protein sequences of a novel
 CC isolated olfactory receptor-like polypeptide, NOVX. The DNA and protein
 CC sequences of the invention and an antibody specific for the protein are
 CC useful for treating or preventing a disorder associated with NOV1 in a
 CC subject, preferably human. A NOVX specific antibody is useful for
 CC determining the presence or amount of protein in a sample. The DNA,
 CC protein and antibody of the invention is useful for diagnosing,
 CC preventing or treating disorders associated with aberrant NOVX expression
 CC such as disorders of olfactory loss, e.g. trauma, human immunodeficiency
 CC virus (HIV) illness, neoplastic growth and neurological disorders, e.g.
 CC Parkinson's disease and Alzheimer's disease. The sequences and NOV
 CC antibody is useful in screening assays, detection assays (e.g.,
 CC chromosomal mapping, tissue typing, forensic biology), predictive
 CC medicine (e.g., diagnostic assays, prognostic assays, monitoring clinical
 CC trials and pharmacogenomic), and in methods of treatment (e.g.,
 CC therapeutic and prophylactic). The NOV protein is useful as immunogen to
 CC produce antibodies immunospecific for the protein, to screen for
 CC potential agonist and antagonist compounds, and as bait protein in a two-
 CC hybrid or three-hybrid assay. The nucleotide sequence is useful in gene
 CC therapy, to express the protein, to detect NOVX mRNA or a genetic lesion
 CC in a NOVX gene, and to modulate NOVX activity. The antibody of the
 CC invention is useful for isolating, and purifying the protein and to
 CC monitor protein levels in tissue as part of a clinical testing procedure.
 CC The present sequence represents the cDNA encoding the NOV7 protein of the
 CC invention
 XX
 SQ Sequence 1008 BP; 216 A; 290 C; 234 G; 268 T; 0 U; 0 Other;
 XX
 Query Match 85.2%; Score 832.4; DB 6; Length 1008;
 Best Local Similarity 91.1%; Pred. No. 2,6e-241;
 Matches 884; Conservative 0; Mismatches 86; Indels 0; Gaps 0;
 QY 8 AAAAAACATCATATGAGGTCGCGAATCCACTTGGGAGAGGCGCTTCACTTGGTGGG 67
 Db 39 AACTACACAGCATGAGCTGTGGAATTCACCTTGGGAGAGTGGCTTCACTTGGTGGG 98

QY 200 CTCCTGCTGGGAGAGCTCTCTCATGAGACCTCTGTTGATCATGTTGTTGACTCTCCCAAG 259
 DB 181 CTCCTGCTGGGAGAGCTCTCTCATGAGACCTCTGTTGATCATGTTGTTGACTCTCCCAAG 240
 QY 260 GCCTTGCGGAGACTTTCTGCGCAGAGAAAACACTATCTCTCTTTGAGAGCTGTCGACTTCAG 319
 DB 241 GCCCTTGCGGAGACTTTCTGCGCAGAGAAAACACTATCTCTCTTTGAGAGCTGTCGACTTCAG 300
 QY 320 ATGTTCTTGCGACTGACATAGGTTAGCGCTGAGAGACTCTTACTGAGCTTCATGAGCTTAT 379
 DB 301 ATGTTCTTGCGACTGACATAGGTTAGCGCTGAGAGACTCTTACTGAGCTTCATGAGCTTAT 360
 QY 380 GACAGGATATGCGCAATTTGTCATCTCTGAAATACATGACCTTCATGAGCTTCAGAGCTC 439
 DB 361 GACAGGATATGCGCAATTTGTCATCTCTGAAATACATGACCTTCATGAGCTTCAGAGCTC 420
 QY 440 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 499
 DB 421 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
 QY 500 ATGTAACATATGACACT 559
 DB 481 GTGTAACATATGACACT 540
 QY 560 ATCCCACTTGTGAGAGTTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 619
 DB 541 ATCCCACTTGTGAGAGTTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 QY 620 GTGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 679
 DB 601 GTGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
 QY 680 GTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 739
 DB 661 ATCTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
 QY 740 TGTCTTCTGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 799
 DB 721 TGTCTTCTGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
 QY 800 TTGCGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 859
 DB 781 TTGCGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
 QY 860 GTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 919
 DB 841 GTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
 QY 920 TTGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 970
 DB 901 TTGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 951
 RESULT 10
 ABZ43126
 ID ABZ43126 standard; DNA; 951 BP.
 AC ABZ43126;
 DT 06-MAR-2003 (first entry)
 DE Human GPCR polynucleotide SEQ ID NO 513.
 DX Human; GPCR; G protein coupled receptor; signal transduction; olfactory;
 KW drug development; gustatory; taste; fragrance; gene; ds.
 OS Homo sapiens.
 PN WO200216548-A2.
 PD 28-FEB-2002.
 PF 30-JUL-2001; 2001WO-1B001446.

XX 04-AUG-2000; 2000JP-00237818.
 PR 13-FEB-2001; 2001JP-00034434.
 XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 PA Haga T, Takeda S, Mitaku S;
 PI WPI; 2002-304118/34.
 DR P-PSDB; ABP95852.
 PT Database global search for G protein-coupled receptors, proteins and
 PT encoded genes for studying in vivo signal transduction mechanism and
 PT identifying targets for drug development.
 PS Claim 9; SEQ ID NO 513; 97pp + Sequence Listing; Japanese.
 CC The invention relates to a method for screening G protein-coupled
 CC receptor (GPCR) genes (ABZ42870-ABZ43216) and/or GPCR proteins (ABP95596-
 CC ABP95942) by extracting open-reading frames containing 6-8 transmembrane
 CC domains with 250-1000 amino acid residues to give a gene homologous with
 CC a known GPCR gene. The receptor proteins and encoded genes are useful for
 CC studying in vivo signal transduction mechanism and identifying targets
 CC for drug development e.g. based on olfactory and gustatory receptors in
 CC form of agonists and antagonists by screening intrinsic and extrinsic
 CC ligands as bitter taste inhibitors, taste enhancers and fragrance
 CC improvers. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pcr_sequences
 XX
 XX Sequence 951 BP; 199 A; 275 C; 218 G; 259 T; 0 U; 0 Other;
 S0
 Query Match 83.9%; Score 819.8; DB 6; Length 951;
 Best Local Similarity 91.4%; Pred. No. 1.7e-237;
 Matches 869; Conservative 0; Mismatches 82; Indels 0; Gaps 0;
 QY 20 ATGAGAGCTCCGGAAGCTCAGCTTGGGAAAGGCGCTTCACTCTGTTGGGGAATCTGAATGAC 79
 DB 1 ATGAGAGCTCCGGAAGCTCAGCTTGGGAAAGGCGCTTCACTCTGTTGGGGAATCTGAATGAC 60
 QY 80 AGTGGGTCTCTGAAAGCTGCTATGCTATGCAATTTCAATTCATATCATTGTTGGGCACTGACC 139
 DB 61 AGTGGGTCTCTGAAAGCTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
 QY 140 AGCAATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 199
 DB 121 AGCAATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
 QY 200 CTCCTGCTGGGAGCTCTCTCTCATGAGAGCTCTCTGTTCAATCTGTTGCTACCTCCAGAG 259
 DB 181 CTCCTGCTGGGAGCTCTCTCTCATGAGAGCTCTCTGTTCAATCTGTTGCTACCTCCAGAG 240
 QY 260 GCCTTGCGGAGCTTTCTGCGCAGAGAAAACACTATCTCTTTGAGAGCTGTCGACTTCAG 319
 DB 241 GCCCTTGCGGAGCTTTCTGCGCAGAGAAAACACTATCTCTTTGAGAGCTGTCGACTTCAG 300
 QY 320 ATGTTCTTGCGACTGACATAGGTTAGCGCTGAGAGACTCTTACTGAGCTTCATGAGCTTAT 379
 DB 301 ATGTTCTTGCGACTGACATAGGTTAGCGCTGAGAGACTCTTACTGAGCTTCATGAGCTTAT 360
 QY 380 GACAGGATATGCGCAATTTGTCATCTCTGAAATACATGACCTTCATGAGCTTCAGAGCTC 439
 DB 361 GACAGGATATGCGCAATTTGTCATCTCTGAAATACATGACCTTCATGAGCTTCAGAGCTC 420
 QY 440 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 499
 DB 421 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
 QY 500 ATGTAACATATGACACT 559
 DB 481 GTGTAACATATGACACT 540
 QY 560 ATCCCACTTGTGAGAGTTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 619

Db 541 ATCCACACTTGTGAGAGTGGCCCTGTGCTGATACCTCCAGATATGAGCTATGATATAT 600
Qy 620 GTGACAGGTGACCTTTCTCTTGTGCTCCCATTTTGTGCAATTTGGCTCTTACACACTA 679
Db 601 GTGATGGGTGACCTTCTCTTATTCCTCTCTGTGCTGATATGAGCTCTCTATACACAA 660
Qy 680 GTCCATATCATGTGCTTGTATGCAATCAATAGAGGAGAGAGAAAGCCCTTGTACCC 739
Db 661 ATTCTACATCATGTGCTTCAATATGCAATCAATAGAGGAGAGAGAAAGCCCTTGTACCC 720
Qy 740 TGCTCTTCCACCTGATTTGTGTCGGAGATGTTCTATGAGAGTGCACATTCATGATATGTC 799
Db 721 TGCTCTTCCACCTGATTTGTGTCGGAGATGTTCTATGAGAGTGCACATTCATGATATGTC 780
Qy 800 TTGGCCAGTCTCTTCCACAGGCCCAACAGACATCATCTCTGTTTCTACACAAAT 859
Db 781 TTGCCAGTCTCTTCCACAGGCCCAACAGACATCATCTCTGTTTCTACACAAAT 840
Qy 860 GTCACTCCAGCCCTGATTCATCATCTATGAGAGTGCACATTCATGATATGTC 919
Db 841 GTCACTCCAGCCCTGATTCATCATCTATGAGAGTGCACATTCATGATATGTC 900
Qy 920 TTGAGAGAGGTCTCTGGAGAAATACATATCTGTCGACATTCACAGCTCTAG 970
Db 901 TTGAGAGAGGTCTCTGGAGAAATACATATCTGTCGACATTCACAGCTCTAG 951

RESULT 11

ABK68461
ID ABK68461 standard; DNA; 951 BP.

AC ABK68461;

DT 02-JUL-2002 (first entry)

DE Human DNA for olfactory and pheromone G protein-coupled receptor #61.

XX Human; ds; gene; olfactory and pheromone G protein coupled receptor;
XX GPCR; tranquilizer; antidepressant; neuroleptic; endocrine; anabolic;
XX anorectic; taste; fragrance; food additive; cosmetic; cell migration;
XX sterility; psychotic disorder; neurological disorder; anxiety;
XX schizophrenia; manic depression; depression; axonal growth;
XX menstrual cycle; appetite sexual motivation; sexual attraction;
XX aggression.

OS Homo sapiens.

PN WO200224726-A2.

PD 28-MAR-2002.

PF 21-SEP-2001; 2001WO-BE000162.

PR 22-SEP-2000; 2000EP-00870211.

PA (CHEM-) CHEMCOM SA.

PI Veichen A;

DR WPI; 2002-330013/36.

DR P-PSDB; AAU95574.

XX Novel pheromone G-protein coupled receptor and receptor-derived agonists,
XX antagonists or inhibitors useful in food or cosmetic products or in the
XX treatment or prevention of neurological disorders such as anxiety and
XX schizophrenia.

XX Disclosure; Page 196-197; 833bp; English.

CC The invention relates to olfactory and Pheromone G-protein coupled
CC receptor (GPCR) or a protein 95% identical to the GPCR, a specific active
CC portion and its encoding polynucleotide. Also included are an agonist.

CC antagonist or inhibitor of the GPCR or the polynucleotide, a vector
CC comprising the polynucleotide, a cell transformed by the vector, a non-
CC human mammal comprising a partial or total deletion of the polynucleotide
CC encoding the receptor and screening (detection and possibly, recovering)
CC of compounds which are known or not known to be agonist, antagonists or
CC inhibitors of natural compounds to the GPCR. The receptor, antagonists or
CC agonists, antagonists, inhibitors or compounds are used as an
CC improvement, elimination or substitution of an existing taste and/or a
CC fragrance of (or in) the food and/or cosmetic products. They can also be
CC used in the preparation of medicament in the treatment and/or prevention
CC of a mammalian disorder, such as cell migration, sterility, psychotic and
CC neurological disorders, including anxiety, schizophrenia, manic
CC depression, depression, for promoting axonal growth, nerve cell
CC connection and nerve regeneration for modulating male and female
CC endocrine functions, hormone production and the menstrual cycle, for the
CC prevention or the treatment by stimulation of several mammalian
CC behaviours, such as stimulation or suppression of appetite, sexual
CC motivation, sexual attraction, aggression and for promoting or
CC suppressing chemical communication between organisms. The present
CC sequence is a human DNA encoding an olfactory and pheromone GPCR
XX

Sequence 951 BP; 199 A; 275 C; 218 G; 259 T; 0 U; 0 Other;

Query Match 83.3%; Score 819.8; DB 6; Length 951;
Best Local Similarity 91.4%; Pred. No. 1.7e-237;
Matches 869; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

Qy 20 ATGAGGTCCTGGAACTCCACCTTGGAGAGCGGCTTCACTTGTGGGAGATTCGATGAC 79
Db 1 ATGAGGTCCTGGAACTCCACCTTGGAGAGCGGCTTCACTTGTGGGAGATTCGATGAC 60
Qy 80 AGTGGTCTCTGAACTGCTCTATGCTATTAACATCTTATACATGTTGGACAGAC 129
Db 61 AGTGGTCTCTGAACTGCTCTATGCTATTAACATCTTATACATGTTGGACAGAC 120
Qy 140 AGCAATGCTGTGCTCTCTGCTGACATACCAATAGAAAGCCGGCTCCACATGCCATGATAC 199
Db 121 AGCAATGCTGTGCTCTCTGCTGACATACCAATAGAAAGCCGGCTCCACATGCCATGATAC 180
Qy 200 CTCCTGCTTGGGAGAGCTCTCTGCTGACATGACCTCTCTGACATCTGTTGATCTCCAG 259
Db 181 CTCCTGCTTGGGAGAGCTCTCTGCTGACATGACCTCTCTGACATCTGTTGATCTCCAG 240
Qy 260 GCTTGGCCGAGCTTCTGCGCAGAGAAACATATCTCTCTTGGAGAGCTGTGACCTGAG 319
Db 241 GCTTGGCCGAGCTTCTGCGCAGAGAAACATATCTCTCTTGGAGAGCTGTGACCTGAG 300
Qy 320 ATGTTCTTGGCACTGACAAATGAGTACGCTGAGGACCTCTTACCTGATGAGGCTAT 379
Db 301 ATGTTCTTGGCACTGACAAATGAGTACGCTGAGGACCTCTTACCTGATGAGGCTAT 360
Qy 380 GACAGGTAATGAGGCAATTTGATCTCTGAAATATACATACCTCTATGAGCCCAAGATC 439
Db 361 GACAGGTAATGAGGCAATTTGATCTCTGAAATATACATACCTCTATGAGCCCAAGATC 420
Qy 440 TGCTGATCATGATGAGCCACATCTGATCTCTGAGATCCCTGATGAGCTATTAAGACATACC 499
Db 421 TGCTGATCATGATGAGCCACATCTGATCTCTGAGATCCCTGATGAGCTATTAAGACATACC 480
Qy 500 ATGTAACATGACCTCTCTTCTGTGTGTCCTGAGAAATGAGGATCTGCTGTGAG 559
Db 481 ATGTAACATGACCTCTCTTCTGTGTGTCCTGAGAAATGAGGATCTGCTGTGAG 540
Qy 560 ATCCACCTCTGAGAAATGAGGCTGATCTGATCTCTGATCTCTGATCTCTGATCTCTGATCT 619
Db 541 ATCCACCTCTGAGAAATGAGGCTGATCTGATCTCTGATCTCTGATCTCTGATCTCTGATCT 600
Qy 620 GTGACAGGTGACCTTCTCTTGTGCTCCCATTTTGTGCAATTTGAGGAGCCCTTACACACTA 679
Db 601 GTGATGGGTGACCTTCTCTTGTGCTCCCATTTTGTGCAATTTGAGGAGCCCTTACACACTA 660
Qy 680 GTCCATATCATGTGCTTGTATGCAATCAATAGAGGAGAGAGAAAGCCCTTGTACCC 739

PR 07-SRP-2000; 2000US-0230732P.
 PR 07-FEB-2001; 2001US-0268682P.
 XX (SENO-) SENOMYX INC.
 XX
 XX Zozulya S;
 XX
 XX WPI; 2001-570867/64.
 DR P-PSDB; AAU24730.
 XX
 XX Nucleic acids encoding human olfactory G protein-coupled receptors,
 PT useful for screening for compounds involved in olfactory sensation, where
 PT the compounds can be used in the food, pharmaceutical and cosmetic
 PT industries to customize odors.
 XX
 XX Claim 1; Page 180; 319pp; English.
 XX
 XX The invention relates to nucleic acids encoding human olfactory
 CC receptors, OR, (a G protein-coupled receptor, GPCR). The OR's
 CC specifically recognise molecules, odourants, that elicit specific
 CC olfactory sensation. The human olfactory receptors and polynucleotides
 CC encoding them are useful for screening a library of chemical compounds
 CC for compounds that are involved in olfactory sensation. Modulators of
 CC their activity are useful for pharmacological and genetic modulation of
 CC olfactory signalling pathways. Therefore, they can be used in the food,
 CC pharmaceutical and cosmetic industries to customise odours and
 CC fragrances. The present sequence encodes a human olfactory receptor of
 CC the invention
 CC
 XX Sequence 975 BP; 189 A; 299 C; 217 G; 270 T; 0 U; 0 Other;
 SQ
 Query March 34.6%; Score 338; DB 5; Length 975;
 Best Local Similarity 61.2%; Pred. No. 1.5e-91;
 Matches 545; Conservative 0; Mismatches 345; Indels 0; Gaps 0;
 QY 52 CTTGATCTTGGGAGGATTTGAAATGACAGTGGGCTTCTGAACTGCTTATGCTAATT 111
 DB 36 CTTGGCTCTACAGGCGCTCATACCCATCGCTCCCGGGCTTCTTGGCAATAGT 95
 QY 112 TACAACTCTATACATGTTGGACAGCAGACGAAATGTTGCTGCTCCGCGCATCAACAT 171
 DB 96 CTTTCACATCTTGGTGGGCTATTAACAGCAACTGGTCATGATTCGTCATCACTACAT 155
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 AC ABZ43145;
 DT 06-MAR-2003 (first entry)
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 DE Human; GPCR; G protein coupled receptor; signal transduction; olfactory;
 KW drug development; gustatory; taste; fragrance; gene; ds.
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 XX Homo sapiens.
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 OS WO200216548-A2.
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 FN 28-FEB-2002.
 PD
 PD 30-JUL-2001; 2001WO-1B001446.
 PF
 PF 04-AUG-2000; 2000JP-00237818.
 PR 13-FEB-2001; 2001JP-00034434.
 XX
 XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 PA
 PA Haga T, Takeda S, Mitaku S;
 PI
 PI WPI; 2002-304118/34.
 DR P-PSDB; ABP95871.
 XX
 XX Database global search for G protein-coupled receptors, proteins and
 PT encoded genes for studying in vivo signal transduction mechanism and
 PT identifying targets for drug development.
 XX
 XX Claim 9; SEQ ID NO 551; 97bp + Sequence Listing; Japanese.
 PS
 PS The invention relates to a method for screening G protein-coupled
 CC receptor (GPCR) genes (ABZ42870-ABZ43216) and/or GPCR proteins (ABP95596-
 CC ABP95942) by extracting open-reading frames containing 6-8 transmembrane
 CC domains with 250-1000 amino acid residues to give a gene homologous with
 CC a known GPCR gene. The receptor proteins and encoded genes are useful for
 CC studying in vivo signal transduction mechanism and identifying targets
 CC for drug development e.g. by screening intrinsinc and extrinsic
 CC form of agonists and antagonists by screening intrinsinc and fragrance
 CC ligands as bitter taste inhibitors, taste enhancers and fragrance
 CC improvers. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
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SQ Sequence 975 BP; 189 A; 299 C; 217 G; 270 T; 0 U; 0 Other;

Query Match 34.6%; Score 338; DB 6; Length 975;

Best Local Similarity 61.2%; Pred. No. 1.5e-91;

Matches 545; Conservative 0; Mismatches 345; Indels 0; Gaps 0;

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Job time : 450 secs

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	LOCUS			
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	ACCESSION	AK016560		
	VERSION	AK016560.1 GI:12855357		
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	SOURCE	Mus musculus (house mouse)		
	ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
	REFERENCE			
	AUTHORS	1 Carninci, P. and Hayashizaki, Y.		
	TITLE	High-efficiency full-length cDNA cloning		
	JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
	MEDLINE	99279253		
	PUBMED	10349636		
	REFERENCE			
	AUTHORS	2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komoh, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.		
	TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
	JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
	MEDLINE	20493974		
	PUBMED	11042159		
	REFERENCE			
	AUTHORS	3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Komoh, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, K., Matsuno, H., Sakaguchi, S., Ikegami, T., Kasaiwagi, K., Fujiwake, K., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.		
	TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer		
	JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
	MEDLINE	20530913		
	PUBMED	11076861		
	REFERENCE			
	AUTHORS	4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.		
	TITLE	Functional annotation of a full-length mouse cDNA collection		
	JOURNAL	Nature 409, 685-690 (2001)		
	REFERENCE			
	AUTHORS	5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.		
	TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs		
	JOURNAL	Nature 420, 563-573 (2002)		
	REFERENCE	6 (bases 1 to 3063)		
	AUTHORS	Adachi, J., Aizawa, K., Akabira, S., Akitamura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Futuda, S., Fukunishi, Y., Furumoto, M., Hanaigaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hironaka, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Itawa, M.,		

	TITLE	JOURNAL						
	Submitted (10-JUN-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 220-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)							
	Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.							
	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAAGACATCCAGAGCTCTTTTCTTTTTTTTNN 3'], cDNA was prepared by using trihalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAAGATTCGTGAATTAAATAAATATCCCCCCCCC 3]. cDNA was cleaved with BamHI and XhoI. cDNA of size compressed longer than 7 kb was selected before cloning. Vector: a modified plasmidscript KS(+) after bulk excision from lambda phi C I. Cloning sites, 5' end: SalI, 3' end: BamHI. Host: DH10B.							
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VERSION AG031161.1 GI:16558034
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AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
TITLE Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,
JOURNAL Totoki, Y., Watanabe, H., and Sakaki, Y.
REFERENCE BAC end sequences of library PTB
AUTHORS Unpublished
TITLE 2 (bases 1 to 710)
JOURNAL Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,
REFERENCE Totoki, Y., Watanabe, H., and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Suenho-chou, Tsunumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: chimpanzee@sc.riken.go.jp, URL: http://hsp.sec.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
COMMENT Clones are derived from the chimpanzee BAC library PTB. This BAC end
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 ORGANISM Pan troglodytes
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 Tokoki, Y., Watanabe, H. and Sakaki, Y.
 BAC end sequences of library PTB
 JOURNAL Unpublished
 AUTHORS 2 (bases 1 to 663)
 TITLE Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
 Tokoki, Y., Watanabe, H. and Sakaki, Y.
 JOURNAL Direct Submission
 Submitted (02-AUG-2001) Aseo Fujiyama, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail: chimpanzee@sc.riken.go.jp, URL: http://hsp.gsc.riken.go.jp/
 Tel: 81-45-503-9111, Fax: 81-45-503-9170)
 Clones are derived from the chimpanzee BAC library PTB. This BAC end
 was generated during the R&D process and may have higher chance of
 clone tracking errors.
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 Best local similarity 91.2%; Pred. No. 9.9e-136;
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QY 203 CTGCTTGGGAGCTCTCTCTCATGAGACCTCTGTTACATCTGTTGCTACTCCCAAGCC 262
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 DB 421 AGGTATGTGGCCATTTGTCTATCTCTGAAATACATGACCTCATGAGCCCAAGCTTGC 480
 QY 443 TGTATCATGTGGGACCATCTGATCTCTGATACCTCTGATGATGCTATATGACATACATG 502
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 DB 541 TACATATGACACCTCCCTTCTGTGTCTCTGAGGAAATCAGGACATCTGCTGTGAGATC 600
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 DEFINITION clone tucclm0125N08 F, genomic survey sequence.
 ACCESSION AZ373068
 VERSION AZ373068.1 GI:10486768
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 REFERENCE 1 (bases 1 to 625)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,
 Irlam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausen, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
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ORIGIN
 Query Match 41.9%; Score 409.2; DB 28; Length 625;
 Best Local Similarity 78.6%; Pred. No. 3.2e-105;
 Matches 489; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

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Qy  GTCACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
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RESULT 6 BY16264 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS

BY16264 968 bp mRNA linear EST 17-DEC-2002
 BY16264 RIKEN full-length enriched, adult male testis Mus musculus
 cDNA clone 493244H21 5', mRNA sequence.
 BY16264
 BY16264.1 GI:27129381
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 968)
 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
 Nishida, I., Otsu, N., Saito, R., Suzuki, H., Yamana, I.,
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 Gariboldi, M., Glasi, C., Godzik, A., Gough, J., Grimmond, S.,
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 Aikawa, T., Fukuda, S., Hara, A., Hashizume, W., Imocani, K., Ishii, Y.,
 Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
 Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,
 Rogers, J., Birney, E. and Hayashizaki, Y.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 22354683
 12466851

TITLE JOURNAL MEDLINE PUBMED COMMENT

Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Saitama-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Carninci, P.,
 Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Horii, F.,
 Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,
 Kondo, S., Kono, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,
 Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N.,
 Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,
 Takeda, Y., Waki, K., Watanabe, K., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Computational Analysis of Full-length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multichannel sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 encyclopedia: real-time sequence clustering for construction of a

QY		392	GCCATTTCATCTCCTCGAATAACATGACCCTCATATGAGGCCCAAGCTCTGGATCATG	451
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ACCESSION				
VERSION				
KEYWORDS				
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ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
PUBMED				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
COMMENT				
FEATURES				

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AY408151

LOCUS
Pan troglodytes HCM3128 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.

ACCESSION
AY408151

VERSION
AY408151.1 GI:39764122

KEYWORDS
GSS.

SOURCE
Pan troglodytes (chimpanzee)

ORGANISM
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.

REFERENCE
1 (bases 1 to 948)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Clivello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios

TITLE
Science 302 (5652), 1960-1963 (2003)

JOURNAL
PUBMED
14671302

REFERENCE
2 (bases 1 to 948)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Clivello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.

COMMENT
Location/Qualifiers

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Best Local Similarity 58.8%; Pred. No. 2.7e-76;
Matches 532; Conservative 0; Mismatches 373; Indels 0; Gaps 0;

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RESULT 10
AY402729

LOCUS
Homo sapiens OR2T10 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.

ACCESSION
AY402729

VERSION
AY402729.1 GI:39758712

KEYWORDS
GSS.

SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 939)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Clivello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios

TITLE
Science 302 (5652), 1960-1963 (2003)

JOURNAL
PUBMED
14671302

REFERENCE
2 (bases 1 to 939)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Clivello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.

COMMENT
Location/Qualifiers

FEATURES
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ORIGIN

Query Match 30.6%; Score 299.4; DB 29; Length 939;
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 Matches 531; Conservative 0; Mismatches 386; Indels 0; Gaps 0;

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Db

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 AK053352
 LOCUS
 DEFINITION

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 homolog [mus musculus], full insert sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

AK053352.1 GI:26343402
 AK053352
 HTC; CAP trapper.
 Mus musculus (house mouse)
 Mus musculus

REFERENCE

1 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)

REFERENCE

2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)

TITLE

3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
 Kono, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,
 Sun, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, K.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)

REFERENCE

4 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
 Kono, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,
 Sun, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, K.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)

TITLE

5 The RIKEN Genome Exploration Research Group Phase II Team and the
 PANTOM Consortium.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)

REFERENCE

6 The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)

TITLE

7 The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)

REFERENCE

8 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
 Fukuda, S., Furum, M., Hanagaki, T., Hara, A., Hashizume, M.,
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hirao, T., Hirozane, T.,
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 Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
 Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,
 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
 Muramatsu, M., and Hayashizaki, Y.
 Direct Submission
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,

TITLE

9 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,

QY

COMMENT

Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.go.jp/
 URL: http://fantom.gsc.riken.go.jp/.
 Location/Qualifiers

FEATURES

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ORIGIN

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RESULT 12

AY408152

AY408152

LOCUS

DEFINITION

Mus musculus Hcm3128 gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.

ACCESSION

AY408152

AY408152.1

GI:39764123

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

REFERENCE

AUTHORS

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
 Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sniensky,J.J.,
 Adams,M.D. and Cargill,M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios

JOURNAL

PUBMED

14671302

2 (bases 1 to 948)

AUTHORS

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JOURNAL

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 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios

TITLE

Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios

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REFERENCE 1 (bases 1 to 2021)
AUTHORS Strausberg, R.
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Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Prepared by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www.shgc.stanford.edu>
Contact: (Dickson, Mark) mcddpaxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
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This clone was selected for full length sequencing because it
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to protein
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ACCESSION

CE644671

VERSION

CE644671.1

KEYWORDS

GSS.

SOURCE

GSS.

ORGANISM

Canis familiaris (dog)

REFERENCE

AUTHORS

TITLE

The dog genome: survey sequencing and comparative analysis

JOURNAL

Science 301 (5641), 1898-1903 (2003)

MEDLINE

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PUBMED

14512627

COMMENT

Contact: Kirkness EF

FEATURES

source

Location/Qualifiers

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Job time : 2527 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 18, 2004, 08:33:28 ; Search time 93 Seconds

(without alignment)
960.054 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1393	87.0	324	5	AAU97928 Novel odo
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6	1390	86.8	316	4	AAG71678 Human olf
7	1390	86.8	316	4	AAU10317 Human olf
8	1390	86.8	316	4	AAU24614 Human olf
9	1390	86.8	316	4	AAU07087 Human odo
10	1390	86.8	316	5	ABP95852 Human GPC
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13	1390	86.8	316	7	ADC85823 Human GPC
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16	833	52.0	317	5	ABB81446 Human GPC
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18	833	52.0	317	6	ABU11174 Human G-P
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28	823.5	51.4	324	4	AAU24730 Human olf
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36	816	50.9	314	4	AAG71902 Human olf
37	816	50.9	314	4	AAE06762 Human G-P
38	816	50.9	314	4	AAU05138 Human odo
39	816	50.9	314	4	AAU24587 Human olf
40	816	50.9	314	5	ABU04025 Human G-P
41	816	50.9	314	5	ABP95895 Human GPC
42	816	50.9	314	5	AAU95551 Human olf
43	816	50.9	314	5	AAU85207 Human olf
44	816	50.9	314	7	ADC86135 Human GPC
45	816	50.9	317	4	AAU05139 Human odo

ALIGNMENTS

RESULT 1
AAG71681
ID AAG71681 standard; protein, 316 AA.

AC AAG71681;
XX
XX
XX 30-JUL-2001 (first entry)
XX
XX
XX Human olfactory receptor polypeptide, SEQ ID NO: 1362.

DE Human olfactory receptor polypeptide, SEQ ID NO: 1362.
XX
XX Human, olfactory receptor; OR; primary scent determination;
KW secondary scent determination; polypeptide library; odour receptor;
KW scent profile; scent fingerprint; scent representation.
XX
XX

OS Homo sapiens.
XX
XX

PN W0200127158-A2.
XX
XX

PD 19-APR-2001.
XX
XX

PF 06-OCT-2000; 2000WO-US027582.
XX
XX

PR 08-OCT-1999; 99US-0158615P.
XX
XX

PK 24-FEB-2000; 2000US-0184809P.
XX
XX

PA (DIGI-) DIGISCENTS.
XX
XX

PA (YEDA) YEDA RES & DEV CO LTD.
XX
XX

PI Bellenson J, Smith D, Lancel D, Glusman G, Fuchs T, Yanai I;
XX
XX

DR WPI; 2001-290713/30.
XX
XX

XX Claim 11; Page 845; 1857pp; English.

The present sequence is an olfactory receptor which is encoded by one of a number of novel polynucleotides. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be

CC used for determining differences in the olfactory faculties of different individuals

XX Sequence 316 AA;

Query Match 100.0%; Score 1602; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 5.5e-167; Mismatches 0; Indels 0; Gaps 0;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELNSTLGGSGFIIIVGIIINDSGSPPELLYATFTIYTMALNTSNGILLAIITTEARLHMPY 60
DB 1 MELNSTLGGSGFIIIVGIIINDSGSPPELLYATFTIYTMALNTSNGILLAIITTEARLHMPY 60
QY 61 LILGQLSLMDLIFTSVTPPKALADPLRENTISFGGCAQMFALTMGSADLLAFMAY 120
DB 61 LILGQLSLMDLIFTSVTPPKALADPLRENTISFGGCAQMFALTMGSADLLAFMAY 120
QY 121 DRYVAICHPKXMTLMSPRVCIMVATSWIIASLAIAGHTWYTMALPCVSWEIRHLICE 180
DB 121 DRYVAICHPKXMTLMSPRVCIMVATSWIIASLAIAGHTWYTMALPCVSWEIRHLICE 180
QY 181 IPIPLKACADTSRYELIIYVGVTFLLPISAIYASTVLVFTVLRMPSNEGKKALVT 240
DB 181 IPIPLKACADTSRYELIIYVGVTFLLPISAIYASTVLVFTVLRMPSNEGKKALVT 240
QY 241 CSSHIIIVGMFGATFMYVLPSSFSHPKODNIIISVFTIYTPALNPLIYSLRNKEVMA 300
DB 241 CSSHIIIVGMFGATFMYVLPSSFSHPKODNIIISVFTIYTPALNPLIYSLRNKEVMA 300
QY 301 LRRVLGKTYILLAHSTL 316
DB 301 LRRVLGKTYILLAHSTL 316

RESULT 2
ID ABB79908 standard; protein; 316 AA.
XX ABB79908;

XX 05-DEC-2002 (first entry)
DE Human olfactory receptor-like protein GPCR1.

XX GPCR1, olfactory receptor; G-protein coupled receptor; receptor; human;
XX antiarteriosclerotic; antidiabetic; analgesic; cytosstatic;
XX antidepressant; nootropic; neuroprotective; immunosuppressive;
XX antiatherogenic; antibacterial; virucide; protozoacide; fungicide;
XX cardiomyopathy; atherosclerosis; diabetes; gene therapy.

OS Homo sapiens.

XX Key Location/Qualifiers
XX FT Domain 41..290
XX FT /note= "7tm_1 domain"

XX WO00270707-AA2.

XX 12-SEP-2002.

XX 18-DEC-2001; 2001WO-US049168.

XX 18-DEC-2000; 2000US-0256635P.

XX (CURA-) CURAGEN CORP.

XX (CORT-) COR THERAPEUTICS INC.

XX Padigaru M., Gerlach V., Smithson G., Stone D., Bin-Yang R.;
XX Conley P., Hart M., Tomlinson JE., Topper UN., Kekuda R., Casman SJ;
XX Edinger S., MacDougall JR;

XX WPI, 2002-698753/75.
XX N-PSDB, ABQ81238.

XX New G-protein coupled receptor (GPCR1) proteins and nucleic acids, useful
PT for treating or preventing a GPCR1-associated disorder, e.g.
PT cardiomyopathy, atherosclerosis, diabetes, or disorders related to cell
PT signal processing.

XX Claim 1; Page 11; 11np; English.

XX The present sequence is the protein sequence of a novel human G-protein
CC coupled receptor, designated GPCR1, that has structural and physiological
CC functions characteristic of the olfactory receptor family, and has
CC properties similar to those of proteins containing the 7tm_1-7
CC transmembrane receptor (rhodopsin family). The invention provides GPCR1
CC polypeptides and nucleic acids, and methods for their recombinant
CC production. These are useful for treating or preventing a GPCR1-
CC associated disorder, such as cardiomyopathy, atherosclerosis, diabetes,
CC or a disorder related to cell signal processing or metabolic pathway
CC modulation in humans (claimed). They may further be used for treating or
CC preventing e.g. developmental diseases, metabolic pathway disorders,
CC retinal disorders, wasting disorders associated with chronic diseases,
CC pain, cancer, psychotic and neurological disorders (e.g. anxiety or
CC schizophrenia), autoimmune diseases, allergies, bacterial, fungal,
CC protozoal and viral infections, neurodegenerative diseases (e.g.
CC Alzheimer's disease), and hematopoietic diseases. The proteins and
CC nucleic acids may also be used as research tools, as diagnostic or
CC prognostic markers, in gene therapy, for promoting tissue regeneration in
CC vitro and in vivo, and as biological defence weapons. The proteins are
CC also are useful for producing antibodies specific for the proteins, as
CC vaccines, and in screening for potential agonists and antagonists

XX Sequence 316 AA;

Query Match 100.0%; Score 1602; DB 5; Length 316;
Best Local Similarity 100.0%; Pred. No. 5.5e-167; Mismatches 0; Indels 0; Gaps 0;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELNSTLGGSGFIIIVGIIINDSGSPPELLYATFTIYTMALNTSNGILLAIITTEARLHMPY 60
DB 1 MELNSTLGGSGFIIIVGIIINDSGSPPELLYATFTIYTMALNTSNGILLAIITTEARLHMPY 60
QY 61 LILGQLSLMDLIFTSVTPPKALADPLRENTISFGGCAQMFALTMGSADLLAFMAY 120
DB 61 LILGQLSLMDLIFTSVTPPKALADPLRENTISFGGCAQMFALTMGSADLLAFMAY 120
QY 121 DRYVAICHPKXMTLMSPRVCIMVATSWIIASLAIAGHTWYTMALPCVSWEIRHLICE 180
DB 121 DRYVAICHPKXMTLMSPRVCIMVATSWIIASLAIAGHTWYTMALPCVSWEIRHLICE 180
QY 181 IPIPLKACADTSRYELIIYVGVTFLLPISAIYASTVLVFTVLRMPSNEGKKALVT 240
DB 181 IPIPLKACADTSRYELIIYVGVTFLLPISAIYASTVLVFTVLRMPSNEGKKALVT 240
QY 241 CSSHIIIVGMFGATFMYVLPSSFSHPKODNIIISVFTIYTPALNPLIYSLRNKEVMA 300
DB 241 CSSHIIIVGMFGATFMYVLPSSFSHPKODNIIISVFTIYTPALNPLIYSLRNKEVMA 300
QY 301 LRRVLGKTYILLAHSTL 316
DB 301 LRRVLGKTYILLAHSTL 316

RESULT 3
ID AAU07088 standard; protein; 324 AA.
XX AAU07088;

XX 24-OCT-2001 (first entry)

XX Human odorant receptor (OR) polypeptide #5.

XX Human, olfactory receptor; OR; G-protein coupled receptor superfamily;
XX GPCR; gene therapy; tranquiliser; vulnerary; anti-HIV; cytosstatic;

KM nootropic; neuroprotective; antiparkinsonian; antiasthmatic; cancer;
 KM antiinflammatory; odorant receptor; olfactory loss; trauma; HIV;
 KW human immunodeficiency virus; neoplastic growth; neurological disorder;
 KM Parkinson's disease; Alzheimer's disease; neurogenesis; Crohn's disease;
 KM wound healing; asthma; Albright hereditary osteodystrophy;
 KM multiple sclerosis; nasal epithelial neuronal tissue; transgenic plant.
 OS Homo sapiens.
 XX MO200157215-A2.
 PN 09-AUG-2001.
 PD 07-FEB-2001; 2001WO-US003923.
 PP 07-FEB-2000; 2000US-0180511P.
 PR 07-FEB-2000; 2000US-0180630P.
 PR 07-FEB-2000; 2000US-0180646P.
 PR 08-FEB-2000; 2000US-0180930P.
 PR 08-FEB-2000; 2000US-0181004P.
 PR 08-FEB-2000; 2000US-0181013P.
 PR 08-FEB-2000; 2000US-0181043P.
 PR 24-JUL-2000; 2000US-0220262P.
 PR 25-JUL-2000; 2000US-0220594P.
 PR 11-AUG-2000; 2000US-0224596P.
 PR 02-NOV-2000; 2000US-0245292P.
 PR 06-FEB-2001; 2001US-0077789.
 XX (CURA-) CURAGEN CORP.
 PA Padigaru M, Spytek KA, Li L, Ballinger RA, Mishra VS;
 PI Baumgartner JC;
 PI MPI; 2001-488883/53.
 DR N-PSDB; AAS11688.
 DR Novel isolated NOVX polypeptide related to human odorant receptor family
 PT of G-protein coupled receptor superfamily of proteins useful for treating
 PT trauma, neoplastic growth, Parkinson's disease, Alzheimer's disease.
 XX
 PS Claim 1; Page 44; 199pp; English.
 CC Novel isolated NOVX polynucleotides and their encoded polypeptides of the
 CC invention are related to the human olfactory (or odorant) receptors
 CC (ORs), from the G-protein coupled receptor (GPCR) superfamily. The
 CC sequences are useful for treating or preventing a pathology associated
 CC with OR in a subject, and for manufacturing a medicament for treating a
 CC syndrome associated with a human disease. These diseases include
 CC disorders of olfactory loss, such as trauma, HIV illness and neoplastic
 CC growth, neurological disorders, such as Parkinson's disease and
 CC Alzheimer's disease, neurogenesis, cancer, wound healing, asthma, Crohn's
 CC disease, multiple sclerosis, and Albright hereditary osteodystrophy. The
 CC polynucleotides and polypeptides are also useful, to identify proteins of
 CC the same family, to screen for molecules which inhibit or enhance the
 CC activity or function of olfactory receptors, to detect nasal epithelial
 CC neuronal tissue, in production of transgenic plants and for the
 CC development of new drug targets for various disorders. This sequence
 CC represents a human OR polypeptide
 XX
 SQ Sequence 324 AA;
 Query Match 87.0%; Score 1393; DB 4; Length 324;
 Best Local Similarity 87.3%; Pred. No. 4.9e-144;
 Matches 276; Conservative 16; Mismatches 24; Indels 0; Gaps 0;

QY 121 DRYVAICHPKMTLMSPRVCMVATSWILASLIALGHMTYTMHLPFCVSMETRIHLCE 180
 DB 129 DRYVAICHPMTMTLMSRACMLVATSWILASLIALYTYTMHPPCRQOELRHLLCE 188
 QY 181 IPEPLKLAADTSRYEILTYTGVPFLLPISAVASYTLVFLYLRAPSNBGRKALVT 240
 DB 189 IPEPLKLAADTSRYEILTYTGVPFLLPISAVASYTLVFLYLRAPSNBGRKALVT 248
 QY 241 CSSHLIVGMFYGATPMYVLPSSFSHPKODNISVFTYITVPALNPLIYSILRNKQVRA 300
 DB 249 CSSHLIVGMFYGATPMYVLPSSFSHTRQDNISVFTYITVPALNPLIYSILRNKQVRA 308
 QY 301 LRRVIGXTYLLAHSTL 316
 DB 309 LRRVIGXTYLLAHSTL 324
 RESULT 4
 AAU97928 standard; protein, 324 AA.
 AAU97928;
 AAU97928; (first entry)
 DT 15-AUG-2002
 DE Novel odourant receptor NOV7 protein.
 KM NOV, odorant receptor; G protein coupled receptor; GPCR; trauma;
 KM olfactory receptor; olfactory loss; neoplastic growth;
 KM human immunodeficiency virus; Alzheimer's disease; HIV;
 KM neurological disorder; Parkinson's disease.
 OS Unidentified.
 XX
 PN WO200236632-A2.
 PD 10-MAY-2002.
 PF 09-OCT-2001; 2001WO-US031744.
 PR 02-NOV-2000; 2000US-0245292P.
 PR 06-FEB-2001; 2001US-0077789.
 PR 20-SEP-2001; 2001US-00245292.
 PA (CURA-) CURAGEN CORP.
 PI Alsobrook JP, Burgess CE, Grose WM, Lepley DM, Padigaru M;
 PI Spytek KA;
 DR MPI; 2002-471499/50.
 DR N-PSDB; ABEK51097.
 PT New isolated olfactory receptor-like polypeptide, NOVX, useful for
 PT diagnosing, preventing or treating disorders of olfactory loss, e.g.
 PT trauma, human immunodeficiency virus illness, neoplastic growth and
 PT neurological disorders.
 XX
 PS Claim 1; Page 34-35; 122pp; English.
 CC This invention relates to the DNA and protein sequences of a novel
 CC isolated olfactory receptor-like polypeptide, NOVX. The DNA and protein
 CC sequences of the invention and an antibody specific for the protein are
 CC useful for treating or preventing a disorder associated with NOVX in a
 CC subject, preferably human. A NOVX specific antibody is useful for
 CC determining the presence or amount of protein in a sample. The DNA,
 CC protein and antibody of the invention is useful for diagnosing,
 CC preventing or treating disorders associated with aberrant NOVX expression
 CC such as disorders of olfactory loss, e.g. trauma, human immunodeficiency
 CC virus (HIV) illness, neoplastic growth and neurological disorders, e.g.
 CC Parkinson's disease and Alzheimer's disease. The sequences and NOV
 CC antibody is useful in screening assays, detection assays (e.g.,
 CC chromosomal mapping, tissue typing, forensic biology), predictive
 CC medicine (e.g., diagnostic assays, prognostic assays, monitoring clinical

CC trials and pharmacogenomic), and in methods of treatment (e.g.,
CC therapeutic and prophylactic). The NOV protein is useful as immunogen to
CC produce antibodies immunospecific for the protein, to screen for
CC potential agonist and antagonist compounds, and as bait protein in a two-
CC hybrid or three-hybrid assay. The nucleotide sequence is useful in gene
CC therapy, to express the protein, to detect NOV mRNA or a genetic lesion
CC in a NOV gene, and to modulate NOV activity. The antibody of the
CC invention is useful for isolating, and purifying the protein and to
CC monitor protein levels in tissue as part of a clinical testing procedure.
CC The present sequence represents the NOV7 protein of the invention.

XX Sequence 324 AA;

Query Match 87.0%; Score 1393; DB 5; Length 324;
Best Local Similarity 87.3%; Pred. No. 4.9e-144; Mismatches 24; Indels 0; Gaps 0;
Matches 276; Conservative 16; Mismatches 24; Indels 0; Gaps 0;

QY 1 MELRNSTLGGFLVGLINDSGSPPELLVATFTIYMLALTSNGLLALATTEARLHMPY 60
DB 9 MELMNFLLGGFLVGLINDSGSPPELLCATITIVYLLALISNGLLALATTEARLHMPY 68
QY 61 LLLGQLSLMDLLFTSVVTPKALADFLRRNTISFGGCAQLMFALTMGSAEDLLAFMAY 120
DB 69 LLLGQLSLMDLLFTSVVTPKALADFLRRNTISFGGCAQLMFALTMGSAEDLLAFMAY 128
QY 121 DRYVAICHPILKXMTLMSPRVCMVATSWILASLAIAGHTMYTMHLPCVSWIEIRHLCE 180
DB 129 DRYVAICHPILKXMTLMSPRVCMVATSWILASLAIAGHTMYTMHLPCVSWIEIRHLCE 188
QY 181 IPEPLKLACADTSRYELIYVGVTELLPISAIYASVTLVLTFTVLRMPSNEGRKKALVT 240
DB 189 IPEPLKLACADTSRYELIYVGVTELLPISAIYASVTLVLTFTVLRMPSNEGRKKALVT 248
QY 241 CSSHLTVGMFGAATFMVYLPSFSFKODNIIISVFTIIVPALNPLIYSLNKEVMA 300
DB 249 CSSHLTVGMFGAATFMVYLPSFSFKODNIIISVFTIIVPALNPLIYSLNKEVMA 308
QY 301 LRRVLGKTYILLASTL 316
DB 309 LRRVLGKTYILLASTL 324

RESULT 5
AAU97927
ID AAU97927 standard; protein; 324 AA.

XX AAU97927;

XX 15-AUG-2002 (first entry)

XX Novel odourant receptor NOV6 protein.

XX NOV, odourant receptor; G protein coupled receptor; GPCR; trauma;
XX olfactory receptor; olfactory loss; neoplastic growth;
XX human immunodeficiency virus; Alzheimer's disease; HIV;
XX neurological disorder; Parkinson's disease.

XX Unidentified.

XX WO200236632-A2.

XX 10-MAY-2002.

XX 09-OCT-2001; 2001WO-US031744.

XX 02-NOV-2000; 2000US-0245292P.

XX 06-FEB-2001; 2001US-00777789.

XX 20-SEP-2001; 2001US-00245292.

XX (CURA-) CURAGEN CORP.

XX Alsedbrook JP, Burgess CE, Grosse WM, Lepley DM, Padigaru M;
PI Splytek KA;

XX WPI; 2002-471499/50.
DR N-P-SDB; ABK53096.

XX New isolated olfactory receptor-like polypeptide, NOVX, useful for
PT diagnosing, preventing or treating disorders of olfactory loss, e.g.
PT trauma, human immunodeficiency virus illness, neoplastic growth and
PT neurological disorders.

PS Claim 1; Page 33; 122pp; English.

XX This invention relates to the DNA and protein sequences of a novel
CC isolated olfactory receptor-like polypeptide, NOVX. The DNA and protein
CC sequences of the invention and an antibody specific for the protein are
CC useful for treating or preventing a disorder associated with NOV1 in a
CC subject, preferably human. A NOVX specific antibody is useful for
CC determining the presence or amount of protein in a sample. The DNA,
CC protein and antibody of the invention is useful for diagnosing,
CC preventing or treating disorders associated with aberrant NOVX expression
CC such as disorders of olfactory loss, e.g. trauma, human immunodeficiency
CC virus (HIV) illness, neoplastic growth and neurological disorders, e.g.
CC Parkinson's disease and Alzheimer's disease. The sequences and NOV
CC antibody is useful in screening assays, detection assays (e.g.,
CC chromosomal mapping, tissue typing, forensic biology), predictive
CC medicine (e.g., diagnostic assays, prognostic assays, monitoring clinical
CC trials and pharmacogenomic), and in methods of treatment (e.g.,
CC therapeutic and prophylactic). The NOV protein is useful as immunogen to
CC produce antibodies immunospecific for the protein, to screen for
CC potential agonist and antagonist compounds, and as bait protein in a two-
CC hybrid or three-hybrid assay. The nucleotide sequence is useful in gene
CC therapy, to express the protein, to detect NOV mRNA or a genetic lesion
CC in a NOV gene, and to modulate NOV activity. The antibody of the
CC invention is useful for isolating, and purifying the protein and to
CC monitor protein levels in tissue as part of a clinical testing procedure.
CC The present sequence represents the NOV6 protein of the invention

XX Sequence 324 AA;

Query Match 87.0%; Score 1393; DB 5; Length 324;
Best Local Similarity 87.3%; Pred. No. 4.9e-144; Mismatches 24; Indels 0; Gaps 0;
Matches 276; Conservative 16; Mismatches 24; Indels 0; Gaps 0;

QY 1 MELRNSTLGGFLVGLINDSGSPPELLVATFTIYMLALTSNGLLALATTEARLHMPY 60
DB 9 MELMNFLLGGFLVGLINDSGSPPELLCATITIVYLLALISNGLLALATTEARLHMPY 68
QY 61 LLLGQLSLMDLLFTSVVTPKALADFLRRNTISFGGCAQLMFALTMGSAEDLLAFMAY 120
DB 69 LLLGQLSLMDLLFTSVVTPKALADFLRRNTISFGGCAQLMFALTMGSAEDLLAFMAY 128
QY 121 DRYVAICHPILKXMTLMSPRVCMVATSWILASLAIAGHTMYTMHLPCVSWIEIRHLCE 180
DB 129 DRYVAICHPILKXMTLMSPRVCMVATSWILASLAIAGHTMYTMHLPCVSWIEIRHLCE 188
QY 181 IPEPLKLACADTSRYELIYVGVTELLPISAIYASVTLVLTFTVLRMPSNEGRKKALVT 240
DB 189 IPEPLKLACADTSRYELIYVGVTELLPISAIYASVTLVLTFTVLRMPSNEGRKKALVT 248
QY 241 CSSHLTVGMFGAATFMVYLPSFSFKODNIIISVFTIIVPALNPLIYSLNKEVMA 300
DB 249 CSSHLTVGMFGAATFMVYLPSFSFKODNIIISVFTIIVPALNPLIYSLNKEVMA 308
QY 301 LRRVLGKTYILLASTL 316
DB 309 LRRVLGKTYILLASTL 324

RESULT 6
AAG71678
ID AAG71678 standard; protein; 316 AA.

XX AAG71678;

XX

DT	30-JUL-2001 (first entry)
DE	Human olfactory receptor polypeptide, SEQ ID NO: 1359.
XX	
KW	Human; olfactory receptor; OR; primary scent determination;
KM	secondary scent determination; polypeptide library; odour receptor;
XX	scent profile; scent fingerprint; scent representation.
OS	Homo sapiens.
PX	MO200127158-A2.
PN	
PD	19-APR-2001.
XX	
PF	06-OCT-2000; 2000WO-US027582.
XX	
PR	08-OCT-1999; 9AUS-0158615P.
XX	24-FEB-2000; 2000US-0184809P.
PA	(DIGI-) DIGISCENTS.
XX	(YEDA) YEDA RES & DEV CO LTD.
PI	Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I,
DR	WPI, 2001-290713/30.
PS	
CC	Claim 11; Page 842-843; 1857pp; English.
CC	The present sequence is an olfactory receptor which is encoded by one of
CC	a number of novel polynucleotides. The polynucleotides can be used in
CC	screening for olfactory agonists and antagonists. The methods allow for
CC	the determination of primary scents and the identification of the odour
CC	receptors used to detect these primary scents. The methods also enable
CC	determination of secondary scents and the identification of combinations
CC	of odour receptors that are involved in detecting such secondary scents.
CC	This enables the construction of a scent representation (also called a
CC	scent fingerprint or scent profile), which may be used to re-create and
CC	edit scents. Libraries of olfactory receptors are useful for determining
CC	the interaction pattern of a composition with the receptors, and can be
CC	used for determining differences in the olfactory faculties of different
CC	individuals
XX	
SQ	Sequence 316 AA;
Query Match:	86.8%; Score 1390; DB 4; Length 316;
Best Local Similarity	87.0%; Pred. No. 1e-143;
Matches 275:	Conservative 17; Mismatches 24; Indels 0; Gaps 0;
OY	1 MELRNSTIGSGFIIIVGILINDSGPELKYATFTIYMALNTSNGILLATTTEARLNHMY 60
DB	1 MEIWNFTIGSGFIIIVGILINDSGPELKYATFTIYLTLINSGLLLATTMEARLNHMY 60
OY	61 LLLGQLSIMDLFFTSVTPPKALADFLRENTISFGGCALQMFLATMGSAEDLLAFMAX 120
DB	61 LLLGQLSIMDLFFTSVTPPKALADFLRENTISFGGCALQMFLATMGAGDULLAFMAX 120
OY	121 DRVAIAICHLKMTLMSPRVGVINAVTSMIIASLIAGHTMYTHMLPCVSWIRHLICE 180
DB	121 DRVAIAICHLPLTYMTLMSRACMWATSWIIASIALITYVMGYPCRAOEIRHLICE 180
OY	181 IPPLLKLACADTSREYELIIVYGTVPLLPISAIIVASTVLPTVLTMPNSNEGRKKALVT 240
DB	181 IPHLKLACADTSREYELIIVYGTVPLLPISAIIVASTVLPTVLTMPNSNEGRKKALVT 240
OY	241 CSHSLIVVGMYGAATMYVLPSSFSHPKODNIISVFYITVPALNPLIYSIRKKEYMRA 300
DB	241 CSHSLIVVGMYGAATMYVLPSSFSHTRODNIIISVFYITVPALNPLIYSIRKKEYMRA 300
OY	301 LRRLVGYTIILAHSTL 316
DB	:::

Db 301 LRRYL6KXMLPAHSTL 316

RESULT 7
AAU10317
ID AAU10317 standard; protein: 316 AA.
AC AAU10317;
XX
DT 25-JAN-2002 (first entry)
DE G-protein coupled receptor (GREC) #18.
XX
KW G-protein coupled receptor; GREC; vaccine; gene therapy;
KW cell proliferation disorder; cancer; arteriosclerosis;
KW neurological disorder; epilepsy; stroke; cardiovascular disorder;
KW hypertension; ischemic heart disease; gastrointestinal disorder;
KW anorexia; peptic ulcer; autoimmune disorder; inflammatory disorder;
KW diabetes; osteoporosis; psoriasis; metabolic disorder; obesity;
KW schizophrenia disorder; neuromuscular disorder.
XX
OS Homo sapiens.
XX
PN MO200166742-A2.
XX
PD 13-SEP-2001.
XX
PF 01-MAR-2001; 2001WO-US006814.
XX
PR 03-MAR-2000; 2000US-0186854P.
PR 10-MAR-2000; 2000US-0188384P.
PR 17-MAR-2000; 2000US-0190453P.
PR 20-MAR-2000; 2000US-0190730P.
XX
PA (INCC-) INCYTE GENOMICS INC.
XX
PI Lal P, Tang YT, Patterson C, Yao MG, Shih LL, Tribouley CM,
PI Lu DM, Yue H, Khan FA, Policky JL, Au-Young J, Yang J, Harland L,
PI Walsh RT, Lo TP, Borowsky ML;
DR N-PESDB; AAS15914.
XX
WP1: 2001-656776/75.

Novel G-protein coupled receptor polypeptides, for treating and preventing autoimmune/inflammatory disorders, neurological disorders, cell proliferative disorders, cardiovascular disorders and viral infections.

Claim 1; Page 128; 141pp; English.

The invention describes a novel isolated polypeptide, selected from a group of 21 G-protein coupled receptor polypeptides (GREC) and useful in vaccines and gene therapy. The polypeptide (I) is useful for screening for agonist or antagonist of (I), compounds specifically binding to (I), or compounds that modulate the activity of (I). The polynucleotide encoding (I) is useful for screening a compound for effectiveness in altering expression of a target polynucleotide comprising (II), by exposing a sample comprising the target polynucleotide to a compound, detecting altered expression of the target polynucleotide, and comparing the expression of the target polynucleotide in the presence of varying amounts of compound and in the absence of the compound. (I) and (II) are useful for diagnosis, treatment and prevention of cell proliferative disorders (e.g. cancers, arthritis, arteriosclerosis, neurodegenerative disorders (e.g. epilepsy, stroke, schizophrenia disorders and neuromuscular disorders), cardiovascular disorders (e.g. hypertension, ischemic heart disease), gastrointestinal disorders (e.g. anorexia, peptic ulcer), autoimmune/inflammatory disorders (e.g. diabetes mellitus, osteoporosis, psoriasis), and metabolic disorders such as obesity).

Furthermore, the polynucleotide is useful, as primers for detecting single nucleotide polymorphisms, as elements in microarray, to monitor or measure protein-protein interactions, drug-target interactions, and gene expression profiles; to generate a transcript image of a tissue or cell type, and to generate hybridization probes useful in mapping the

CC naturally occurring genomic sequence. This is the G-protein coupled
 CC receptor 18 (GPRC-18), one of 21 GPCR proteins described in the method
 CC of the invention

XX SQ Sequence 316 AA;

Query Match 86.8%; Score 1390; DB 4; Length 316;
 Best Local Similarity 87.0%; Pred. No. 1e-143;

Matches 275; Conservative 17; Mismatches 24; Indels 0; Gaps 0;

QY 1 MELRNSTLGGFLLVGLINDSGSPDLLATFTLLMALTNSGILLATITTEARLHMPY 60
 DB 1 MELRNFTLGGFLLVGLINDSGSPDLLATITLLYLLALISNGILLATITTEARLHMPY 60
 QY 61 LLLGQSLMDLFTSVTPRALADFLRENTISFGGALOMFLATIMGAEEDLLAFMAY 120
 DB 61 LLLGQSLMDLFTSVTPRALADFLRENTISFGGALOMFLATIMGAEEDLLAFMAY 120
 QY 121 DRYVAIGHPLKMYTLMSPRCWIMVATSWILASLIAIGHTMYTMHLPCVSWEIRHLICE 180
 DB 121 DRYVAIGHPLKMYTLMSPRCWIMVATSWILASLIAIGHTMYTMHLPCVSWEIRHLICE 180
 QY 181 IPPLLKACADTSRYELIIVYTGVTFLLPISAVASYTLVLTVMPSNEGRKKALVT 240
 DB 181 IPPLLKACADTSRYELIIVYTGVTFLLPISAVASYTLVLTVMPSNEGRKKALVT 240
 QY 241 CSSHLYVGMFYGAATMYVLPSSFHSPKODNIISVFYITVPALNPLIYSLRNKEVWRA 300
 DB 241 CSSHLYVGMFYGAATMYVLPSSFHSPKODNIISVFYITVPALNPLIYSLRNKEVWRA 300
 QY 301 LRRVLGKXYTLIAHSTL 316
 DB 301 LRRVLGKXYTLIAHSTL 316

RESULT 8

AAU24614 ID AAU24614 standard; protein; 316 AA.

XX AC AAU24614;

XX DT 18-DEC-2001 (first entry)

XX DE Human olfactory receptor AOLFRL07.

XX KW Human; olfactory receptor; G protein-coupled receptor; GPCR; odourant;
 KW food additive; cosmetic; fragrance; pharmaceutical additive.

XX OS Homo sapiens.

XX PN WO200168805-A2.

XX PD 20-SEP-2001.

XX PF 13-MAR-2001; 2001WO-US007771.

XX PR 13-MAR-2000; 2000US-0188914P.

XX PR 24-MAR-2000; 2000US-0192033P.

XX PR 12-APR-2000; 2000US-0198474P.

XX PR 24-APR-2000; 2000US-0199335P.

XX PR 26-MAY-2000; 2000US-0207702P.

XX PR 23-JUN-2000; 2000US-0213849P.

XX PR 16-AUG-2000; 2000US-0226534P.

XX PR 07-SEP-2000; 2000US-0230732P.

XX PR 07-FEB-2001; 2001US-0266862P.

XX PA (SENO-) SENOMYX INC.

XX PI Zozulya S;

XX DR WPI, 2001-570867/64.

XX DR N-PSDB; AAS42307.

PT Nucleic acids encoding human olfactory G protein-coupled receptors,
 PT useful for screening for compounds involved in olfactory sensation, where
 PT the compounds can be used in the food, pharmaceutical and cosmetic
 PT industries to customize odors.

XX PS Claim 60; Page 127; 319pp; English.

XX CC The invention relates to nucleic acids encoding human olfactory
 CC receptors, OR, (a G protein-coupled receptor, GPCR). The OR's
 CC specifically recognise molecules, odourants, that elicit specific
 CC olfactory sensation. The human olfactory receptors and polynucleotides
 CC encoding them are useful for screening a library of chemical compounds
 CC for compounds that are involved in olfactory sensation. Modulators of
 CC their activity are useful for pharmacological and genetic modulation of
 CC olfactory signalling pathways. Therefore, they can be used in the food,
 CC pharmaceutical and cosmetic industries to customise odours and
 CC fragrances. The present sequence is a human olfactory receptor of the
 CC invention

XX SQ Sequence 316 AA;

Query Match 86.8%; Score 1390; DB 4; Length 316;
 Best Local Similarity 87.0%; Pred. No. 1e-143;

Matches 275; Conservative 17; Mismatches 24; Indels 0; Gaps 0;

QY 1 MELRNSTLGGFLLVGLINDSGSPDLLATFTLLMALTNSGILLATITTEARLHMPY 60
 DB 1 MELRNFTLGGFLLVGLINDSGSPDLLATITLLYLLALISNGILLATITTEARLHMPY 60
 QY 61 LLLGQSLMDLFTSVTPRALADFLRENTISFGGALOMFLATIMGAEEDLLAFMAY 120
 DB 61 LLLGQSLMDLFTSVTPRALADFLRENTISFGGALOMFLATIMGAEEDLLAFMAY 120
 QY 121 DRYVAIGHPLKMYTLMSPRCWIMVATSWILASLIAIGHTMYTMHLPCVSWEIRHLICE 180
 DB 121 DRYVAIGHPLKMYTLMSPRCWIMVATSWILASLIAIGHTMYTMHLPCVSWEIRHLICE 180
 QY 181 IPPLLKACADTSRYELIIVYTGVTFLLPISAVASYTLVLTVMPSNEGRKKALVT 240
 DB 181 IPPLLKACADTSRYELIIVYTGVTFLLPISAVASYTLVLTVMPSNEGRKKALVT 240
 QY 241 CSSHLYVGMFYGAATMYVLPSSFHSPKODNIISVFYITVPALNPLIYSLRNKEVWRA 300
 DB 241 CSSHLYVGMFYGAATMYVLPSSFHSPKODNIISVFYITVPALNPLIYSLRNKEVWRA 300
 QY 301 LRRVLGKXYTLIAHSTL 316
 DB 301 LRRVLGKXYTLIAHSTL 316

RESULT 9

AAU07087 ID AAU07087 standard; protein; 316 AA.

XX AC AAU07087;

XX DT 24-OCT-2001 (first entry)

XX DE Human odorant receptor (OR) polypeptide #4.

XX KW Human; olfactory receptor; OR; G-protein coupled receptor superfamily;
 KW GPCR; gene therapy; tranquilliser; vulnerary; anti-HIV; cytostatic;
 KW neurotropic; neuroprotective; antiparkinsonian; antistimetic; cancer;
 KW antiinflammatory; odorant receptor; olfactory loss; trauma; HIV;
 KW human immunodeficiency virus; neoplastic growth; neurological disorder;
 KW Parkinson's disease; Alzheimer's disease; neurogenesis; Crohn's disease;
 KW wound healing; asthma; Albigright hereditary osteodysplrophy;
 KW multiple sclerosis; nasal epithelial neuronal tissue; transgenic plant.

XX OS Homo sapiens.

XX PN WO200157215-A2.

PD 09-AUG-2001.
 XX 07-FEB-2001; 2001WO-US003923.
 PF
 XX 07-FEB-2000; 2000US-0180511P.
 PR 07-FEB-2000; 2000US-0180630P.
 PR 07-FEB-2000; 2000US-0180646P.
 PR 08-FEB-2000; 2000US-0180930P.
 PR 08-FEB-2000; 2000US-0181004P.
 PR 08-FEB-2000; 2000US-0181013P.
 PR 08-FEB-2000; 2000US-0181043P.
 PR 24-JUL-2000; 2000US-0220262P.
 PR 25-JUL-2000; 2000US-0220534P.
 PR 11-AUG-2000; 2000US-0224536P.
 PR 02-NOV-2000; 2000US-0245232P.
 PR 06-FEB-2001; 2001US-00777789.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Padigaru M, Spytek KA, Li L, Ballinger RA, Mishra VS,
 PI Baumgartner JC;
 XX WPI, 2001-488883/53.
 DR N-PSDB; AAS11687.
 DR
 XX
 PT Novel isolated NOVX polypeptide related to human odorant receptor family
 PT of G-protein coupled receptor superfamily of proteins useful for treating
 PT trauma, neoplastic growth, Parkinson's disease, Alzheimer's disease.
 XX
 PS Claim 1; Page 39; 199pp; English.
 XX
 CC Novel isolated NOVX polynucleotides and their encoded polypeptides of the
 CC invention are related to the human olfactory (or odorant) receptors
 CC (ORs), from the G-protein coupled receptor (GPCR) superfamily. The
 CC sequences are useful for treating or preventing a pathology associated
 CC with OR in a subject, and for manufacturing a medicament for treating a
 CC syndrome associated with a human disease. These diseases include
 CC disorders of olfactory loss, such as trauma, HIV illness and neoplastic
 CC growth, neurological disorders, such as Parkinson's disease and
 CC Alzheimer's disease, neurogenesis, cancer, wound healing, asthma, Crohn's
 CC disease, multiple sclerosis, and Abright hereditary osteodysplrophy. The
 CC polynucleotides and polypeptides are also useful to identify proteins of
 CC the same family, to screen for molecules which inhibit or enhance the
 CC activity or function of olfactory receptors, to detect nasal epithelial
 CC neuronal tissue, in production of transgenic plants and for the
 CC development of new drug targets for various disorders. This sequence
 CC represents a human OR polypeptide
 CC
 XX
 SQ Sequence 316 AA;
 Query Match 86.8%; Score 1390; DB 4; Length 316;
 Best Local Similarity 87.0%; Pred. No. 1e-143;
 Matches 275; Conservative 17; Mismatches 24; Indels 0; Gaps 0;
 QY 1 MELRNSTGSGFIVGLINDSGPELVATFTILYMLALTSNGLLATTTARLAMPY 60
 DB 1 MELRNFTGSGFIVGLINDSGPELVATFTILYMLALTSNGLLATTTARLAMPY 60
 QY 61 LILGOLSLMDLFTSVTPKALADFLRRENTISFGSCALQMFALATMGSAEDLLAFMAY 120
 DB 61 LILGOLSLMDLFTSVTPKALADFLRRENTISFGSCALQMFALATMGSAEDLLAFMAY 120
 QY 121 DRYVAICHPILKMTLMSRVCWIMVATSWILASLAIAGHTMYTWMHPGVSWEIRHLCE 180
 DB 121 DRYVAICHPILKMTLMSRVCWIMVATSWILASLAIAGHTMYTWMHPGVSWEIRHLCE 180
 QY 181 IPIPLAKACADTSRELIIVYGVTELLPISAIYASTVLVFTULRMSNNGRKALVT 240
 DB 181 IPIPLAKACADTSRELIIVYGVTELLPISAIYASTVLVFTULRMSNNGRKALVT 240
 QY 241 CSSHLIVGMFYGAATFMVILPSSFSHPKODNIISVFYTIYTPALNPLIYSIRNENVRA 300
 DB 241 CSSHLIVGMFYGAATFMVILPSSFSHPKODNIISVFYTIYTPALNPLIYSIRNENVRA 300

QY 301 LRRVLGKXITLAAHSTL 316
 DB 301 LRRVLGKXITLAAHSTL 316
 RESULT 10
 ID ABP95852 standard; protein; 316 AA.
 ABP95852
 AC ABP95852;
 XX
 DT 06-MAR-2003 (first entry)
 XX
 DE Human GPCR polypeptide SEQ ID NO 514.
 XX
 KW Human; GPCR; G protein coupled receptor; signal transduction; olfactory;
 KW drug development; gustatory; taste; fragrance; receptor.
 OS Homo sapiens.
 XX
 EN WO200216548-A2.
 PD 28-FEB-2002.
 PF 30-JUL-2001; 2001WO-IB001446.
 PR 04-AUG-2000; 2000JP-00237818.
 PR 13-FEB-2001; 2001JP-00034434.
 XX
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 XX
 PI Haga T, Takeda S, Mitaku S;
 PI WPI, 2002-304118/34.
 DR N-PSDB; ABZ43126.
 DR
 XX
 PT Database global search for G protein-coupled receptors, proteins and
 PT encoded genes for studying in vivo signal transduction mechanism and
 PT identifying targets for drug development.
 XX
 PS Claim 10; SEQ ID NO 514; 97pp + Sequence Listing; Japanese.
 XX
 CC The invention relates to a method for screening G protein-coupled
 CC receptor (GPCR) genes (ABZ4870-ABZ43126) and/or GPCR proteins (ABP95596-
 CC ABP95942) by extracting open-reading frames containing 6-8 transmembrane
 CC domains with 250-1000 amino acid residues to give a gene homologous with
 CC a known GPCR gene. The receptor proteins and encoded genes are useful for
 CC studying in vivo signal transduction mechanism and identifying targets
 CC for drug development e.g. based on olfactory and gustatory receptors in
 CC form of agonists and antagonists by screening intrinsic and extrinsic
 CC ligands as bitter taste inhibitors, taste enhancers and fragrance
 CC improvers. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIP0 at ftp.wipo.int/pub/published_pct_sequences
 CC
 XX
 SQ Sequence 316 AA;
 Query Match 86.8%; Score 1390; DB 5; Length 316;
 Best Local Similarity 87.0%; Pred. No. 1e-143;
 Matches 275; Conservative 17; Mismatches 24; Indels 0; Gaps 0;
 QY 1 MELRNSTGSGFIVGLINDSGPELVATFTILYMLALTSNGLLATTTARLAMPY 60
 DB 1 MELRNFTGSGFIVGLINDSGPELVATFTILYMLALTSNGLLATTTARLAMPY 60
 QY 61 LILGOLSLMDLFTSVTPKALADFLRRENTISFGSCALQMFALATMGSAEDLLAFMAY 120
 DB 61 LILGOLSLMDLFTSVTPKALADFLRRENTISFGSCALQMFALATMGSAEDLLAFMAY 120
 QY 121 DRYVAICHPILKMTLMSRVCWIMVATSWILASLAIAGHTMYTWMHPGVSWEIRHLCE 180
 DB 121 DRYVAICHPILKMTLMSRVCWIMVATSWILASLAIAGHTMYTWMHPGVSWEIRHLCE 180

QY 181 IPEPLKLAACADTSRYELIIYVTGTPLLPISAVSYTLVFTVLRMPSEGRKKALVT 240
 DB 181 IPEPLKLAACADTSRYELIIYVTGTPLLPISAVSYTLVFTVLRMPSEGRKKALVT 240
 QY 241 CSSHLIVGMFYGAATPMYVLPSSFSFKODNIIISVYTTVTPALNPLIYSLRNKEVWRA 300
 DB 241 CSSHLIVGMFYGAATPMYVLPSSFSFKODNIIISVYTTVTPALNPLIYSLRNKEVWRA 300
 QY 301 LRRVLGKYILLAHSTL 316
 DB 301 LRRVLGKYILLAHSTL 316
 RESULT 11
 AAU95574 standard; protein; 316 AA.
 AAU95574;
 02-JUL-2002 (first entry)
 Human olfactory and pheromone G protein-coupled receptor #61.
 Human; olfactory and pheromone G protein coupled; receptor; GPCR;
 tranquilizer; antidepressant; neuroleptic; endocrine; anabolic;
 anorectic; taste; fragrance; food additive; cosmetic; cell migration;
 sterility; psychotic disorder; neurological disorder; anxiety;
 schizophrenia; manic depression; depression; axonal growth;
 menstrual cycle; appetite sexual motivation; sexual attraction;
 aggression.
 Homo sapiens.
 WO200224726-A2.
 28-MAR-2002.
 21-SEP-2001; 2001WO-BE000162.
 22-SEP-2000; 2000EP-00870211.
 (CHEM-) CHEMCOM SA.
 Veithen A;
 WPI; 2002-330013/36.
 N-PSDB; ABK68461.
 Novel pheromone G-protein coupled receptor and receptor-derived agonists,
 antagonists or inhibitors useful in food or cosmetic products or in the
 treatment or prevention of neurological disorders such as anxiety and
 schizophrenia.
 Disclosure; Page 197-198; 833pp; English.

CC endocrine functions, hormone production and the menstrual cycle, for the
 CC prevention or the treatment by stimulation of several mammalian
 CC behaviours, such as stimulation or suppression of appetite, sexual
 CC motivation, sexual attraction, aggression and for promoting or
 CC suppressing chemical communication between organisms. The present
 CC sequence is a human olfactory and pheromone GPCR protein sequence
 XX
 SQ Sequence 316 AA;
 Query Match 86.8%; Score 1390; DB 5; Length 316;
 Best Local Similarity 87.0%; Pred. No. 1e-143;
 Matches 275; Conservative 17; Mismatches 24; Indels 0; Gaps 0;
 QY 1 MELRNSTLGSGLIVGLINDSGSPPELLVATFTLLYMLALTSNGLLALITTEARLHMPY 60
 DB 1 MELRNSTLGSGLIVGLINDSGSPPELLVATFTLLYMLALTSNGLLALITTEARLHMPY 60
 QY 61 LILGQSLMDLFTSVTPRALADFLRRENTISFGGALCMFLATMGSAEDLLAFMAY 120
 DB 61 LILGQSLMDLFTSVTPRALADFLRRENTISFGGALCMFLATMGSAEDLLAFMAY 120
 QY 121 DRYVAICHPLKNTLMSPRVCWIMVATSWILASLIGHMTYTMHLPCVSWETRHLCE 180
 DB 121 DRYVAICHPLKNTLMSPRVCWIMVATSWILASLIGHMTYTMHLPCVSWETRHLCE 180
 QY 181 IPEPLKLAACADTSRYELIIYVTGTPLLPISAVSYTLVFTVLRMPSEGRKKALVT 240
 DB 181 IPEPLKLAACADTSRYELIIYVTGTPLLPISAVSYTLVFTVLRMPSEGRKKALVT 240
 QY 241 CSSHLIVGMFYGAATPMYVLPSSFSFKODNIIISVYTTVTPALNPLIYSLRNKEVWRA 300
 DB 241 CSSHLIVGMFYGAATPMYVLPSSFSFKODNIIISVYTTVTPALNPLIYSLRNKEVWRA 300
 QY 301 LRRVLGKYILLAHSTL 316
 DB 301 LRRVLGKYILLAHSTL 316
 RESULT 12
 AAU85234
 ID AAU85234 standard; protein; 316 AA.
 AAU85234;
 08-MAY-2002 (first entry)
 G-coupled olfactory receptor #95.
 Human; olfactory G-coupled receptor; sensory perception of odourant;
 odour composition; taste composition.
 Homo sapiens.
 WO200198526-A2.
 27-DEC-2001.
 22-JUN-2001; 2001WO-US020122.
 22-JUN-2000; 2000US-0213812P.
 13-MAR-2001; 2001US-00804291.
 (SENO-) SENOMYX INC.
 Zozulya S, Stryer L;
 WPI; 2002-083330/11.
 N-PSDB; ABK37593.
 Representing sensory perception of one or more odorants for the
 PT identification and design of tastes and odors comprises providing a
 PT representative group of n olfactory receptors.
 XX

PS Claim 1; Page 101; 182pp; English.

XX The invention relates to a method of representing sensory perception of
CC one or more odourants. The method comprises: (a) providing a
CC representative class of n olfactory receptors or ligand binding domains
CC (LBD) of these receptors; (b) measuring values X1 to Xn representative of
CC at least one activity of one or more odourants selected from: (i) binding
CC one or more odourants to the LBD of at least one of the n olfactory
CC receptors; (ii) activating at least one of the n olfactory receptors with
CC the one or more odourants; and (iii) blocking at least one of the n
CC olfactory receptors with the one or more odourants; and (c) generating a
CC representation of the sensory perception of odourants is useful for the
CC design and formulation of the sensory perception of odourants. AAUS5140-AAUS3393
CC represent human olfactory G-coupled receptor amino acid sequences of the
XX invention

XX Sequence 316 AA;

Query Match 86.8%; Score 1390; DB 5; Length 316;
Best Local Similarity 87.0%; Pred. No. 1e-143;

Matches 275; Conservative 17; Mismatches 24; Indels 0; Gaps 0;

QY 1 MEIRNSTLGSGLVINGLINDSGSPDLATFTLLVMTALTSNGLLATITTEARLHPMY 60
DB 1 MEIRNSTLGSGLVINGLINDSGSPDLATFTLLVMTALTSNGLLATITTEARLHPMY 60
QY 61 LILGQSLMDLFTSVTPPALADFLRENTISFGGALOMFLATMGAEIDLAFMAY 120
DB 61 LILGQSLMDLFTSVTPPALADFLRENTISFGGALOMFLATMGAEIDLAFMAY 120
QY 121 DRYVALCHPLKWTMTSPRCWIMVATSWIASLAIAGHTMTYMHLPFCVSMERHLC 180
DB 121 DRYVALCHPLKWTMTMTSSRAQMLVATSWIASLAIAGHTMTYMHLPFCVSMERHLC 180
QY 181 IPPLKACADTSRYELIIVYGVTELLPISAVASYTLVLTFLVMPSPNEKRKALVT 240
DB 181 IPPLKACADTSRYELIIVYGVTELLPISAVASYTLVLTFLVMPSPNEKRKALVT 240
QY 241 CSNHLIVGMFYGAATFMVLPSSFHSFKODNIIISVFTYITVPALNPLIYSLNKEWMRA 300
DB 241 CSNHLIVGMFYGAATFMVLPSSFHSFKODNIIISVFTYITVPALNPLIYSLNKEWMRA 300
QY 301 LRRVLGKTYLLAHSTL 316
DB 301 LRRVLGKTYLLAHSTL 316

RESULT 13

ADC85823
ID ADC85823 standard; protein; 316 AA.

XX ADC85823;

DT 01-JAN-2004 (first entry)

DE Human GPCR protein SEQ ID NO:276.

KW human; GPCR; guanosine triphosphate-binding protein coupled receptor;
KM gene therapy.

XX Homo sapiens.

OS Homo sapiens.

PN EP1270724-A2.

PD 02-JAN-2003.

PF 18-JUN-2002; 2002EP-00013517.

PR 18-JUN-2001; 2001JP-00246789.

PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

XX Suwa M, Asai K, Akiyama Y, Aburatani H;
XX WPI; 2003-315783/31.
DR N-PSDB; ADC85822.

XX New polynucleotide, useful for preparing a composition for treating a
PT patient in need of increased or suppressed activity or expression of the
PT guanosine triphosphate-binding protein coupled receptor.

PS Claim 2; SEQ ID NO 276; 28pp; English.

XX The invention relates to a novel polynucleotide encoding a guanosine
CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
CC the invention may have a use in gene therapy. The polynucleotide and
CC polypeptide are useful for preparing a composition for treating a patient
CC in need of increased or suppressed activity or expression of the
CC guanosine triphosphate-binding protein coupled receptor. The protein
CC sequences shown in ADC8549-ADC87617 represent GPCR's of the invention.

XX Sequence 316 AA;

Query Match 86.8%; Score 1390; DB 7; Length 316;
Best Local Similarity 87.0%; Pred. No. 1e-143;

Matches 275; Conservative 17; Mismatches 24; Indels 0; Gaps 0;

QY 1 MEIRNSTLGSGLVINGLINDSGSPDLATFTLLVMTALTSNGLLATITTEARLHPMY 60
DB 1 MEIRNSTLGSGLVINGLINDSGSPDLATFTLLVMTALTSNGLLATITTEARLHPMY 60
QY 61 LILGQSLMDLFTSVTPPALADFLRENTISFGGALOMFLATMGAEIDLAFMAY 120
DB 61 LILGQSLMDLFTSVTPPALADFLRENTISFGGALOMFLATMGAEIDLAFMAY 120
QY 121 DRYVALCHPLKWTMTSPRCWIMVATSWIASLAIAGHTMTYMHLPFCVSMERHLC 180
DB 121 DRYVALCHPLKWTMTMTSSRAQMLVATSWIASLAIAGHTMTYMHLPFCVSMERHLC 180
QY 181 IPPLKACADTSRYELIIVYGVTELLPISAVASYTLVLTFLVMPSPNEKRKALVT 240
DB 181 IPPLKACADTSRYELIIVYGVTELLPISAVASYTLVLTFLVMPSPNEKRKALVT 240
QY 241 CSNHLIVGMFYGAATFMVLPSSFHSFKODNIIISVFTYITVPALNPLIYSLNKEWMRA 300
DB 241 CSNHLIVGMFYGAATFMVLPSSFHSFKODNIIISVFTYITVPALNPLIYSLNKEWMRA 300
QY 301 LRRVLGKTYLLAHSTL 316
DB 301 LRRVLGKTYLLAHSTL 316

RESULT 14

ABB81447
ID ABB81447 standard; protein; 317 AA.

XX ABB81447;

DT 28-AUG-2002 (first entry)

DE Human GPCR4b protein sequence SEQ ID NO:16.

KW Human; GPCR; G protein-coupled receptor; antihypertensive;
KM anorectic; antibacterial; fungicide; protozoacide; vinuclide; analgesic;
KM cytostatic; immunomodulator; metabolic; antidiabetic; antiparkinsonian;
KM hypertensive; hypotensive; osteopathic; antidiabetic; anti-HIV;
KM antidiabetic; neuroprotective; antiangiogenic; cardioprotective;
KM antiallergic; nootropic; tranquilizer; neuroleptic; antidepressant;
KM antianemic; anticonvulsant; haemostatic; immunosuppressive; hepatotropic;
KM cerebroprotective; dermatological; antidiabetic; gynaecological; cancer;
KM nephroprotective; gene therapy; vaccine; developmental disease; diabetes;
KM cardiomyopathy; atherosclerosis; neurodegenerative disorder;
KM autoimmune disorder; infectious disease; chromosome 1.

CC fragrances. The present sequence is a human olfactory receptor of the
CC invention
XX
SQ Sequence 317 AA;

Query Match 52.0%; Score 833; DB 4; Length 317;
Best Local Similarity 50.5%; Pred. No. 1.4e-82;
Matches 156; Conservative 57; Mismatches 96; Indels 0; Gaps 0;

```
QY 1 MEARNSTLIGSGFIIIVGILINDSGPELIVATFTILYMLALTSNGLLLATITTEARLHMPY 60
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 1 MEQSNYSVYADFIILGLFSNARFPMLLFALILVFLTSIASNVVKIILIHIDSRHPTMY 60
QY 61 LLLGQLSIMDLFTSVVTPKALADFLRRENTISFGGALQMFALITMGSAEDLLLPAY 120
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 61 FLLSQLSIRDLIVSTIVPKALVDQVMSQRAISFAGCTAOHFILYTLTLAGAEFFLLGLMSY 120
QY 121 DRYVAICHPLKYMTLMSPRVCMIMWATSWILASLIAIHTWYTMHLPECVSWEIRHLCE 180
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 121 DRYVAICNPLHYPLMSRKICMLIVAAAWLGGSIDGFLTPVTMOPFCASREINHFCE 180
QY 181 IPELKLACADTSRELIIVYTGVTFLLPISALVASYTLVLFVTLMPSNEGRKKALVT 240
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 181 VPALLKLSCTDTSAYETAMVCCIMMLIPFSVISGSYTRILITVYMSSEABGRKAVAT 240
QY 241 CSSHLIYVGMFYGAATPMYVLPSSFHSPKODNTISVYTTVTPALNPLIYSLRNKEVMRA 300
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 241 CSSHMVYVSLFYGLAMTYTVLPHSYHTPEODKAVSAFYTLITPMLNPLIYSLRNKDVYGA 300
QY 301 LRRVLGKYI 309
   |||:::|||||
Db 301 LQKVVGRCV 309
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Search completed: August 18, 2004, 08:56:44
Job time : 96 secs

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OM protein - protein search, using sw model

Run on: August 18, 2004, 08:37:43 ; Search time 16 Seconds

(without alignments)
1899.783 Million cell updates/sec

Title: US-10-024-444B-2

Sequence: 1 MEARNSTLGSGLVNGIAND.....VNRALRRVLGKTLAHSTL 316

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 78:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	632	43.2	315	2	JC5836	olfactory receptor
2	684	42.7	312	2	A46247	olfactory receptor
3	672	41.9	311	2	JC5200	chemoreceptor TR33
4	670.5	41.9	309	1	S51356	olfactory receptor
5	668.5	41.7	313	2	S20571	olfactory receptor
6	659	41.1	316	2	A57069	olfactory receptor
7	653.5	40.9	305	2	S29711	olfactory factor O
8	648	40.4	314	2	A37286	olfactory receptor
9	644	40.2	314	2	S29707	olfactory receptor
10	641	40.0	314	2	H23701	olfactory receptor
11	640	40.0	304	2	S29709	olfactory receptor
12	634	39.6	310	2	E23701	olfactory receptor
13	632	39.5	314	2	S20572	olfactory receptor
14	622	38.8	313	2	B23701	olfactory receptor
15	621	38.8	312	2	123701	olfactory receptor
16	614.5	38.4	312	2	A48413	probable olfactory
17	608	38.0	312	2	S29708	olfactory receptor
18	600.5	37.5	320	2	S20573	olfactory receptor
19	592	37.0	312	2	G23701	olfactory receptor
20	588	36.7	315	2	JC5201	chemoreceptor TR56
21	588	36.7	319	2	JC5624	chemoreceptor
22	587.5	36.6	327	2	F23701	olfactory receptor
23	587	36.6	318	2	JC5202	chemoreceptor
24	576	36.0	333	2	A23701	olfactory receptor
25	565.5	35.3	307	2	S29710	olfactory receptor
26	564	35.2	315	2	JC4658	olfactory receptor
27	542.5	33.9	317	2	D23701	olfactory receptor
28	532	33.2	264	2	PC4369	olfactory receptor
29	528.5	33.0	311	2	C23701	olfactory receptor

30	523	32.6	312	2	A46750	olfactory receptor
31	496.5	31.0	222	2	D40745	odorant receptor (
32	476	29.7	157	2	S58033	probable olfactory
33	476	29.7	216	2	I38481	olfactory receptor
34	471	29.4	157	2	S58019	probable olfactory
35	467	29.2	157	2	S58029	probable olfactory
36	465	29.0	157	2	S58037	probable olfactory
37	462	28.8	157	2	S58073	probable olfactory
38	457	28.5	216	2	I38470	olfactory receptor
39	453	28.3	216	2	I38474	olfactory receptor
40	450	28.1	222	2	E40745	odorant receptor (
41	448.5	28.0	225	2	I38478	olfactory receptor
42	431	26.9	234	2	S28999	G protein-coupled
43	426	26.6	232	2	S29001	G protein-coupled
44	424	26.5	234	2	S28998	G protein-coupled
45	423.5	26.4	328	2	G45774	odorant receptor 2

ALIGNMENTS

RESULT 1

JC5836
Olfactory receptor-like protein 2 - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 05-Mar-1998 #sequence_revision 13-Mar-1998 #text_change 24-Nov-1999
C/Accession: JC5836
R/Biochem. Biophys. Res. Commun. 242, 669-672, 1998
A/Title: Cloning and tissue distribution of a new rat olfactory receptor-like (OL2).
A/Reference number: JC5836; PMID:98125551; EMD:9464275
A/Accession: JC5836
A/Status: nucleic acid sequence not shown
A/Molecule type: DNA
A/Residues: 1315 <BLA>
A/Cross-references: GB:AF029357; NID:92570934; PIDN:AAC39969.1; PID:92570935
C/Comment: This protein is implicated in white cell muturation and migration.
C/Superfamily: olfactory receptor OR14
F/28-53/Domain: transmembrane #status predicted <TM1>
F/64-96/Domain: transmembrane #status predicted <TM2>
F/95-123/Domain: transmembrane #status predicted <TM3>
F/147-165/Domain: transmembrane #status predicted <TM4>
F/203-229/Domain: transmembrane #status predicted <TM5>
F/241-264/Domain: transmembrane #status predicted <TM6>
F/277-293/Domain: transmembrane #status predicted <TM7>

Query Match 43.2%; Score 692; DB 2; Length 315;

Best Local Similarity 44.4%; Pred. No. 1.6e-51;
Matches 134; Conservative 65; Mismatches 103; Indels 0; Gaps 0;

QY	5	NTLGSGLVNGIANDSGSPDLVATFTLVMTALNSGLLLATITEARLHPVLLIG 64	
DB	8	NSSVSERFLILPPSSSQRLMALFFLLVYLLVGLNGSLVALLVLDRLTPWPFPS 67	
QY	65	QSLMDLFTSVVTPKALADFLRRNTISFGCALQMFALTMGSAEDLLAFMAYDRYV 124	
DB	68	ILSLVDMSVYTTVPQMLVNWVCPRKTTISWGACVQMFFIVLIGIECVLXMAADRYI 127	
QY	125	ALCHPLKTKTTLSPRYCVMTMATSILASLAIIGHRTYTMHLPRCVSMETRIHLGIPDI 184	
DB	128	ALCFPLHVSVLMSRIVCAVMVTICSSIVTGLALIVTVFTMLPYCGPYKINHFCEVPVAV 187	
QY	185	LKLAQADTSRYELIIVTVGTFLLPISAIIVASYTLVLTFTVLRMPENGRKKALVCCSH 244	
DB	188	LKLAQADTSFNRDLPIIFGLVLLVPLSLILMSYACIFSLIRINSQGRLLSFTCSAH 247	
QY	245	LIVGMPFYGAATFMYVLDPSSFSHPKQDNIISVYITVTPALNPLVLSLNKEVMRALREV 304	
DB	248	ITVVTMFYGPAMVMTMRPGSVYDPRDKKALFYNNVSAFLNPIITSLNNKVKAGFMKV 307	
QY	305	LG 306	
DB	308	LG 309	


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Db      59 PMYFELSLSPVDLCYSTVITPKMLVNFGLKGNKITTSCEMAQGFPAIPVTECYLLTV 118
Qy      118 MAYRYVALCHPLKMYTLMSPRVCMVWVAVSWIILAIQHTMYTMEPCVSWEIRHL 177
Db      119 MAYDRYVALCHPLKMYTLMSPRVCMVWVAVSWIILAIQHTMYTMEPCVSWEIRHL 178
Qy      178 LCEIPPLKACADTSREYELIIVYGVTFLLPISALVASTYLVLFVTLRMPSEGRKKA 237
Db      179 FCDMLPLKACADTSREYELIIVYGVTFLLPISALVASTYLVLFVTLRMPSEGRKKA 238
Qy      238 LVTCSHLLVGMFGAATFMYVLPSSFSHPKODNIISVFYITVPALNPLIYSIRKKEV 297
Db      239 FGCTSSHLMAVGIFFGSITTMYLKRPSSNSLDEKSVSEYITVIVPLNPLIISLRKXDV 298
Qy      298 LRRRLR 303
Db      299 KKALGR 304

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RESULT 5

olfactory receptor - dog
 C/Species: Canis lupus familiaris (dog)
 C/Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 26-Aug-1999
 C/Accession: S20571
 R/Parmentier, M.; Libert, F.; Schurmans, S.; Schiffmann, S.; Lefort, A.; Eggerickx, D.; Nature 355, 453-455, 1992
 A/Title: Expression of members of the putative olfactory receptor gene family in mammal
 A/Reference number: S20571, MUID:9213132, PMID:1370859
 A/Accession: S20571
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-313 <PAR>
 A/Cross-references: EMBL:X64996; NID:9890; PIDN:CAA46129.1; PID:9891
 C/Suprafamily: olfactory receptor OR14
 C/Keywords: G protein-coupled receptor; transmembrane protein

```

Query Match      41.7%; Score 668.5; DB 2; Length 313;
Best Local Similarity 42.6%; Pred. No. 1.6e-49;
Matches 130; Conservative 60; Mismatches 114; Indels 1; Gaps 1;

Qy      1 MELRNTLGSGLFVINGLINDSGSPPELLYAFITLMLALNSGLLALITTEARLHPMY 60
Db      1 MTEKNTVSEFVLGLGPIPDQORDLFTALFLAMYVTLIGNLITVLQLDSHLTPMY 60
Qy      61 LLLGQLSLMDLFTSVVTPKALADFLRRENTISFGGCAIQMFLATMGSAEDLLAFMAY 120
Db      61 LFLSNLSFSDLCSSVTMPKRLQNMOSQVPSIPYACLTQMVFLEFGDLESTLVAMAY 120
Qy      121 DRVVAICHPLKMYTLMSPRVCMVWVAVSWIILAIQHTMYTMEPCVSWEIRHLCE 180
Db      121 DRVVAICHPLEHYTTIMSPKLSLAVSWLTFMFHVAHTLIMARLCFCAN-TIPFFCD 179
Qy      181 IPEPLKACADTSREYELIIVYGVTFLLPISALVASTYLVLFVTLRMPSEGRKKA 240
Db      180 MSALTKLACSDTQVNELVLFIMGGLIVLPFLIITISYARISYSLKVPASAGICVCFST 239
Qy      241 CSSHLLVGMFGAATFMYVLPSSFSHPKODNIISVFYITVPALNPLIYSIRKKEVMA 300
Db      240 CGSHLSVSLVLFYGYTGLYLCPSANNSYKETTMMATVIVPLNPLIYSIRKCKMCA 299
Qy      301 LRRRLR 305
Db      300 LRRRLR 304

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RESULT 6

olfactory receptor Part1 - human
 C/Species: Homo sapiens (man)
 C/Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 26-Aug-1999
 C/Accession: A57069

R/Fan, W.; Liu, Y.C.; Parimoo, S.; Weissman, S.M.
 Genomics 27, 119-123, 1995
 A/Title: Olfactory receptor-like genes are located in the human major histocompatibility
 A/Reference number: A57069; MUID:95394447; PMID:7665158
 A/Accession: A57069
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-316 <FAN>
 A/Cross-references: GB:L35475; NID:g1041044; PIDN:AA836567.1; PID:g601919
 C/Genetics:
 A/Gene: GDB:FAT11; OLF2
 A/Cross-references: GDB:1323249; OMIM:600578
 A/Map position: 6p21.3-6p21.3
 C/Suprafamily: olfactory receptor OR14

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Query Match      41.1%; Score 659; DB 2; Length 316;
Best Local Similarity 40.1%; Pred. No. 1e-48;
Matches 123; Conservative 72; Mismatches 110; Indels 2; Gaps 1;

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Qy      1 MELRNTLGSGLFVINGLINDSGSPPELLYAFITLMLALNSGLLALITTEARLHPMY 60
Db      1 MDNQSSFT--PGFLLDFSEHPGLGRITLVFVDTISYLLTVGNLTLLIISLMDTKLSPMY 58
Qy      61 LLLGQLSLMDLFTSVVTPKALADFLRRENTISFGGCAIQMFLATMGSAEDLLAFMAY 120
Db      59 FFLSNLSFSDLCFTSCVPMLANLWGPCKTISFLDCSVQIFLFLSIGTECIIMKVMAF 118
Qy      121 DRVVAICHPLKMYTLMSPRVCMVWVAVSWIILAIQHTMYTMEPCVSWEIRHLCE 180
Db      119 DRVVAICHPLEHYTTIMSPKLSLAVSWLTFMFHVAHTLIMARLCFCAN-TIPFFCD 178
Qy      181 IPEPLKACADTSREYELIIVYGVTFLLPISALVASTYLVLFVTLRMPSEGRKKA 240
Db      179 VPALIRLSCEDSYNINQVAVSVFLVPLSLIVSYGAILTAVLRINSATMKRAFGT 238
Qy      241 CSSHLLVGMFGAATFMYVLPSSFSHPKODNIISVFYITVPALNPLIYSIRKKEVMA 300
Db      239 CGSHLLVVTLLFYSSVAVLQPNPYAQGRKFGFLFVAVGFPSPINPLVYTLANKKIKRA 298
Qy      301 LRRRLR 307
Db      299 LRRRLR 305

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RESULT 7

olfactory factor OR37 - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 04-Sep-1998
 C/Accession: S29711
 R/Ramming, K.; Krieger, J.; Strotmann, J.; Boekhoff, I.; Kubic, S.; Baumtark, C.; Breer
 Nature 361, 353-356, 1993
 A/Title: Cloning and expression of odorant receptors.
 A/Reference number: S29707; MUID:93149273; PMID:7678922
 A/Accession: S29711
 A/Molecule type: mRNA
 A/Residues: 1-305 <RAM>
 C/Suprafamily: olfactory receptor OR14

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Query Match      40.9%; Score 655.5; DB 2; Length 305;
Best Local Similarity 44.0%; Pred. No. 2e-48;
Matches 136; Conservative 54; Mismatches 102; Indels 17; Gaps 6;

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Qy      13 ILVGLINDSGSP--ELVATFT--IIMYALTNGSLLLALITTEARLHPMYLLIGQLSM 69
Db      1 LLLGL--SGPKTILIFVIVLVYHTNGVLLIISIPDSHLTPMYEPFLNLSFL 57
Qy      70 DILFTSVVTPKALADFLRRENTISFGGCAIQMFLATMGSAEDLLAFMAYRYVAICHP 129
Db      58 DICYTTSSVPSITVSLIKKRNISFGCTGVQFVGFANAGSTECCLLGMMAFRRYVAICHP 117
Qy      130 LKMYTLMSPRVCMVWVAVSWIILAIQHTMYTMEPCVSWEIRHLCEIPEPLKAC 189

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Db 118 LRSVMSKEVYVSMASWFSGGINSVQTSIAMLRLPCGNVYINHFTCEVLAVLKAC 177
 QY 190 ADTSRRELIYVTGVTFLLPIGAIYASITLVLPVLRMSNGRKAALVTCSSHLIVG 249
 Db 178 ADISLNVTVIVNISMMELVPLLIIFPSYVLIYTLIRNMSASGRRAVSTCSAHLTVV 237
 QY 250 MFPGATFMVTVLPS-----FHSFKQDNISVFYITVTPALNPLIYSIRNKEVRAAL 301
 Db 238 IFPGTFSMAKPSQSOLTKDKRQGT--SDKIISLFYGVVTPMLNPITISLRNDVAAV 295
 QY 302 RRVL-GKXI 309
 Db 296 KYLIKQXI 304

RESULT 8
 A37286
 Olfactory receptor 115 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-Aug-1999
 C:Accession: A37286
 R:Buck, L.; Axel, R.
 Cell 65, 175-187, 1991
 A:Title: A novel multigene family may encode odorant receptors: a molecular basis for od
 A:Reference number: A23701; MUID:91191556; PMID:1840504
 A:Accession: A37286
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-314 <BUC>
 A:Cross-references: GB:M64392; NID:g205845; PIDN:AAA4175.1; PID:g205846
 C:Superfamily: olfactory receptor OR14
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 40.4%; Score 648; DB 2; Length 314;
 Best Local Similarity 41.7%; Pred. No. 8.8e-48;
 Matches 128; Conservative 59; Mismatches 120; Indels 0; Gaps 0;

QY 1 MELNSTLGSGLIVGILNDGSPFLIYATFTIYMLALTSNGLLAITTEARLHMPY 60
 Db 1 MTERNQTVISQFLILGPIPEHQHVYALFLSMYLTITLGNLIITLIILDSHLHTPMY 60
 QY 61 LILGOLSIMDLFTSVVTPKALADFLRENTISFGCALQMFALTWGSABDLIAFMAY 120
 Db 61 LFLNLSFSDLCFSSVTMPKILQNMGSQVPSIPFAGCLTQLYFYLVFADLESFLLVAMAY 120
 QY 121 DRYVAICFPLHYMSIMSPKLCVSLVLSWVLTTFHAMHTLIMARLSFCADNMIPIHFCD 180
 Db 121 DRYVAICFPLHYMSIMSPKLCVSLVLSWVLTTFHAMHTLIMARLSFCADNMIPIHFCD 180
 QY 181 IPLLKLIACADTSRELIYVTGVTFLLPIGAIYASITLVLPVLRMSNGRKAALVT 240
 Db 181 ISPLKLSGSDTRVNEELVFMGGLVIVIPFLIIVSARVAVASLTKPVSQGIHKIST 240
 QY 241 CSHSLIVGMFYGATFMVLPSSFHSFKQDNISVFYITVTPALNPLIYSIRNKEVRA 300
 Db 241 CGSHLSVSLFYGITIGIYLCPSANNSVYKETVMMMTVTPMLNPFIYSLRNDMKEA 300
 QY 301 LRRVLGK 307
 Db 301 LIRVLCK 307

RESULT 9
 S29707
 Olfactory receptor OR5 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 26-Aug-1999
 C:Accession: S29707; B37286
 R:Raming, K.; Krieger, J.; Strocmann, J.; Boehhoff, I.; Kubick, S.; Baumstark, C.; Breez
 Nature 361, 353-356, 1993
 A:Title: Cloning and expression of odorant receptors.
 A:Reference number: S29707; MUID:93149273; PMID:7678922
 A:Accession: S29707

A:Molecule type: mRNA
 A:Residues: 1-314 <RAM>
 R:Buck, L.; Axel, R.
 Cell 65, 175-187, 1991
 A:Title: A novel multigene family may encode odorant receptors: a molecular basis for od
 A:Reference number: A23701; MUID:91191556; PMID:1840504
 A:Accession: B37286
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 193-236 <BUC>
 A:Cross-references: GB:M64375; NID:g205811; PIDN:AAA41738.1; PID:g205812
 C:Superfamily: olfactory receptor OR14
 C:Keywords: G protein-coupled receptor; membrane protein

Query Match 40.2%; Score 644; DB 2; Length 314;
 Best Local Similarity 40.4%; Pred. No. 1.9e-47;
 Matches 124; Conservative 66; Mismatches 117; Indels 0; Gaps 0;

QY 1 MELNSTLGSGLIVGILNDGSPFLIYATFTIYMLALTSNGLLAITTEARLHMPY 60
 Db 1 MTERNQTVISQFLILGPIPEHQHVYALFLSMYLTITLGNLIITLIILDSHLHTPMY 60
 QY 61 LILGOLSIMDLFTSVVTPKALADFLRENTISFGCALQMFALTWGSABDLIAFMAY 120
 Db 61 LFLNLSFSDLCFSSVTMPKILQNMGSQVPSIPFAGCLTQLYFYLVFADLESFLLVAMAY 120
 QY 121 DRYVAICFPLHYMSIMSPKLCVSLVLSWVLTTFHAMHTLIMARLSFCEDNVIPIHFCD 180
 Db 121 DRYVAICFPLHYMSIMSPKLCVSLVLSWVLTTFHAMHTLIMARLSFCEDNVIPIHFCD 180
 QY 181 IPLLKLIACADTSRELIYVTGVTFLLPIGAIYASITLVLPVLRMSNGRKAALVT 240
 Db 181 MSALLKLACSDTRVNEELVFMGGLVIVIPFLIIVSARVAVASLTKPVSQGIKAFSS 240
 QY 241 CSHSLIVGMFYGATFMVLPSSFHSFKQDNISVFYITVTPALNPLIYSIRNKEVRA 300
 Db 241 CGSHLSVSLFYGITIGIYLCPSANNSVYKETVMMMTVTPMLNPFIYSLRNDIKGA 300
 QY 301 LRRVLGK 307
 Db 301 MEIIFCK 307

RESULT 10
 H23701
 Olfactory receptor 19 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-Aug-1999
 C:Accession: H23701
 R:Buck, L.; Axel, R.
 Cell 65, 175-187, 1991
 A:Title: A novel multigene family may encode odorant receptors: a molecular basis for od
 A:Reference number: A23701; MUID:91191556; PMID:1840504
 A:Accession: H23701
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-314 <BUC>
 A:Cross-references: GB:M64388; NID:g205837; PIDN:AAA4175.1; PID:g205838
 C:Superfamily: olfactory receptor OR14
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 40.0%; Score 641; DB 2; Length 314;
 Best Local Similarity 40.4%; Pred. No. 3.5e-47;
 Matches 124; Conservative 62; Mismatches 121; Indels 0; Gaps 0;

QY 1 MELNSTLGSGLIVGILNDGSPFLIYATFTIYMLALTSNGLLAITTEARLHMPY 60
 Db 1 MTERNQTVISQFLILGPIPEHQHVYALFLSMYLTITLGNLIITLIILDSHLHTPMY 60
 QY 61 LILGOLSIMDLFTSVVTPKALADFLRENTISFGCALQMFALTWGSABDLIAFMAY 120
 Db 61 LFLNLSFSDLCFSSVTMPKILQNMGSQVPSIPFAGCLTQLYFYLVFADLESFLLVAMAY 120

Query 121 DRVVALCHPLKXMTLSPKRCIMVATSWILASLIAIGHWTYTMHLPRCVSWEIRHLCE 180
Db 121 DRVVALCHPLKXMTLSPKRCIMVATSWILASLIAIGHWTYTMHLPRCVSWEIRHLCE 180
181 IPPLKLACADTSRYELIIVYGVTFLLPISAVASYTLVLFVLRMPNSNEGRKKALVT 240
181 MSTLLKVCAGSDTHDNEALFILGGPIVLPFLILIVSARIVYSIFKPPSSGSIHKAFST 240
QY 241 CSHSLIVGVNFMFYGAATFMYVLPSSFSHPKQDNIIISVFYTIYTPALNPLIYSLRNKRVMA 300
241 CSHSLIVSVSLFYGVIVGLYLCPSANNSTYKETWISLMTYVTPMLNPLIYSLRNDIDKA 300
QY 301 LRRVGLCK 307
Db 301 LERIKMCK 307

RESULT 11
S29709
Olfactory receptor OR14 - rat
CISpecies: Rattus norvegicus (Norway rat)
CDate: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 04-Sep-1998
CAccession: S29709
R.Raming, K.; Krieger, J.; Stroctmann, J.; Boekhoff, I.; Kudick, S.; Baumstark, C.; Bree
A>Title: Cloning and expression of odorant receptors.
A:Reference number: S29707; MUID:93149273; PMID:7678922
A:Accession: S29709
A:Molecule type: mRNA
A:Residues: 1-304 <RAM>
C:Superfamily: olfactory receptor OR14

Query Match 40.0%; Score 640; DB 2; Length 304;
Best Local Similarity 43.5%; Pred. No. 4.1e-47;
Matches 130; Conservative 53; Mismatches 116; Indels 0; Gaps 0;

QY 12 FILVGLINDSGPELLVATFTILYMLALTSNGLLLAITTEARLHMPYLLIGLSLMDL 71
Db 5 FILAGLTDQGLMPLFEFLFGFYMTVGNLIGFLGLINSHLHTPMYFFLENLVYDF 64
QY 72 LFTSVVTPRALDPLRENTISFGGCALOWFLALTMGSAEDLLAFMYADRVVALCHPLK 131
Db 65 CFSSTIIPKMLMSFISKNTIISHSGMTQLFPCFPVVSFTPLISAMAYDRVVALCNPLM 124
QY 132 VMTLSPRCVIMVATSWILASLIAIGHWTYTMHLPRCVSWEIRHLCEIPPLKLACAD 191
Db 125 YIVTMSPOVCLLLILGAVVWGFSEMAHTGMLMUTFCADLVNHPMCDILPBLEISGNS 184
QY 192 TSYRELIIVYGVTFLLPISAVASYTLVLFVLRMPNSNEGRKKALVTCSSHLIVGVN 251
Db 185 TFINELVFIIVADIAVPIVSIPISYALILSLIRHSTGRSKAFSTCSSHLIVCLL 244
QY 252 YGAATFMYVLPSSFSHPKQDNIIISVFYTIYTPALNPLIYSLRNKRVMAALRRVGLCKYL 310
Db 245 FSGGAFMYLKLPSILPLPDQKVSLLFYTIIVPMNLPLIYSLRNDKVVALRRTLGKIL 303

RESULT 12
E23701
Olfactory receptor I3 - rat
CISpecies: Rattus norvegicus (Norway rat)
CDate: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-Aug-1999
CAccession: E23701
R.Buck, L.; Axel, R.
A>Title: A novel multigene family may encode odorant receptors: a molecular basis for od
A:Reference number: A23701; MUID:91191556; PMID:1840504
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-310 <RUC>
C:Superfamily: olfactory receptor OR14

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match	39.6%; Score 634; DB 2; Length 310;
Best Local Similarity	38.9%; Pred. No. 1.3e-46;
Matches 118; Conservative 69; Mismatches 116; Indels 0; Gaps 0;	
QY	3 LRNSTLGGSPFLVGLINDSGSPPELLVYATFTLLYMLALTSNGLLDLATITEARLHPMYLL 62
DB	1 MNNQTFITQFLILGLPIPEEHQHLFYALFLVMYLTLLIGNLLIIVLQDSQALHPMYLF 60
QY	63 LGSLLMDLFTSVVTPKALADFLURENTTISFGGCAQLMFALATMGSAEDLLAFMAYDR 122
DB	61 LSNLSFSLDCSSVTMRKLQNMRSQDTSIYGGCLAQTYFPFMFGDSEFLVAMAYDR 120
QY	123 YVAICHPLPKTYLMTSPRVCTIMVATSWITLAILAIGHTMYTMHLPECVSWEIRHLCEIP 182
DB	121 YVALCFPLHTYSIMSPKCTCTCLVLLMWLTTSHAMMHLLAARLSFCENNVAVLNFCDL 180
QY	183 PLKTIACADTSRYELLIVTGVTFLLLPISAIIVASYTLVLTFLRMPSENGRKALVTC 242
DB	181 VLLKLACSDTYINELMIFIMSTLLIIPFLIVMSYARIISILKVPSTQICKVFTSG 240
QY	243 SHLIYVGMFYGAALFMYLVLPSSFSFKODNIIISFYITVTPALNPLIISLNKKEVMRLR 302
DB	241 SHLSVSLFYGIIIGLYCLCPAGNNSTVKEVMAMMYIVTVMINDPFIISLRNDMKRALI 300
QY	303 RVL 305
DB	301 RVI 303

```

RESULT 13
S20572
Olfactory receptor - human
C,Species: Homo sapiens (man)
C,Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 26-Aug-1999
C,Accession: S20572
R,Parmentier, M.; Libert, F.; Schumans, S.; Schiffmann, S.; Lefort, A.; Eggerickx, D.;
Nature 355, 443-445, 1992
A,Title: Expression of members of the putative olfactory receptor gene family in mammal
A,Reference number: S20571, MUID:92131132, PMID:1370859
A,Accession: S20572
A,Status: preliminary
A,Molecule type: nucleic acid
A,Residues: 1-314 <PAR>
A,Cross-references: EMBL:X64994; NID:g32085; PION:CAA46127.1; PID:g32086
C,Superfamily: olfactory receptor OR14
C,Keywords: G protein-coupled receptor; transmembrane protein

Query Match          39.5%; Score 632; DB 2; Length 314;
Best Local Similarity 41.4%; Pred. No. 2e-46;
Matches 125; Conservative 57; Mismatches 120; Indels 0; Gaps 0;

QY 4 RNSTIGSFILVGLINDSGPELLYATFTLLYMLALTJNSGILLATITEARLHMPMYLL 63
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 4 QNQTISDFLLGLPTIOPEQONLCALFLAYVLTLLCNLLIYIRDSHPTMYFL 63
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 64 GOLSLMDLFTSVTPKALADFLRENTISGGCALQWFLATWMSADLLLAFAAYDRY 123
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 64 SNLSPSDLCFSSVTIPKLLQNMQNDPSIPYADCLTQWYFLLFGDLESFLLVMAAYDRY 123
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 124 VALGHEPLKMTLMSRVCMIVATSWTILASLAIQHTMYTHLPRCVSEIIRHLCELRP 183
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 124 VALGHEPLKMTLMSRVCMIVATSWTILASLAIQHTMYTHLPRCVSEIIRHLCELRP 183
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 184 LKLAACADTSREYELIYVTGVFLPLPISAVASYTLVFLVRLMPSNEGRRKALVTGSS 243
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 184 LKLAACADTSREYELIYVTGVFLPLPISAVASYTLVFLVRLMPSNEGRRKALVTGSS 243
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 244 HLIVVGMRYGAATFMYVLPSSFHSKQNDIISVFTIYTPNLPLIYSLRKVEYRARLR 303
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 244 HLIVVGMRYGAATFMYVLPSSFHSKQNDIISVFTIYTPNLPLIYSLRKVEYRARLR 303
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

QY	304	VL	305
		:	
Db	304	VI	305

RESULT 14

Olfactory receptor F5 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 04-Sep-1998
C:Accession: B23701
R:Buck, L.; Axel, R.
Cell 65, 175-187, 1991
A:Title: A novel multigene family may encode odorant receptors: a molecular basis for
A:Reference number: A23701, MUID:91191556, PMID:1840504
A:Accession: B23701
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-313 <BUC>
A:Cross-references: GB:M64377
C:Superfamily: olfactory receptor OR14
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match	38.8%;	Score 622;	DB 2;	Length 313;
Best Local Similarity	40.3%;	Pred. No. 1.4e-45;		
Matches 123;	Conservative 55;	Mismatches 127;	Indels 0;	Gaps 0;

[illegible]

RESULT 15

Olfactory receptor 114 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-Aug-1999
C:Accession: 123701
R:Buck, L.; Axel, R.
Cell 65, 175-187, 1991
A:Title: A novel multigene family may encode odorant receptors: a molecular basis for od
A:Reference number: A23701, MUID:91191556, PMID:1840504
A:Accession: 123701
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-312 <BUC>
A:Cross-references: GB:W64391, NID:G205843, PIDD:AAA41754.1, PID:G205844
C:Superfamily: olfactory receptor OR14
Keywords: G protein-coupled receptor; transmembrane protein

Query Match	38.8%	Score 621;	DB 2;	Length 312;
Best Local Similarity	41.5%;	Pred. No. 1.7e-45;		
Matches 125;	Conservative 55;	Mismatches 121;	Indels 0;	Gaps 0;

```

QY 5 N0TL5G5FLVINGLND5G5PELLVATPEITLVMALNTSGILLALITTEARLHAMMYLLIG 64
Db 5 N0QL1EEFL5GLPI5PE5EYHLLFVLFAMVLTIIIGLGLITIVLRD5SHLHMEWYLF5 64
QY 65 QLSIMDLFT5VTPKALADFLARENTISFGCALOMFLATMG5AEDILAFADRYV 124
Db 65 NLSF5DLCS5TMRPLLOM5QVPS15TGCLTQLYFPV5FGDM5FL1VMAYDRYV 124
QY 125 A1CHPLKWTLMSPRVCWIMVAT5N1IASL1AGHTWYMHLPFCV5WEIRHLLCE1PPL 184
Db 125 A1CFPLARTITINSTKRCASVLVLLMLMTHALHTHTLLIARL5CEKNVLIHPFCDISAL 184
QY 185 LK1ACADT5ERYELL1YVGVTFLL1P1SAIYASITVL1FVLRMP5NEGRKALVTC5H 244
Db 185 LK1SCSD1DVNE1M1Y1IGL1111PFL1VMSYVR1F55ILKEP51OD1KVF5TG5H 244
QY 245 L1YV5G5GATPMVVL5BSF5SPKODI15EPTI1VTPALNPL1YSLRN5EWRALRV 304
Db 245 L5VVT1LFYGL1FG1Y1CP5GNN5T5YK1AMAMMTV1VPM1NPL1YSLRNDKMRALRV 304
QY 305 I 305
Db 305 I 305

```

Search completed: August 18, 2004, 08:59:04
Job time : 17 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2004, 08:34:28 ; Search time 13 Seconds

(without alignment)
1265.705 Million cell updates/sec

Title: US-10-024-444B-2

Sequence: 1 MBLRSTGSGFTLVGLIND.....VRLRLRVLGKTIILAHSTL 316

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1390	86.8	316	1	O2AG_HUMAN
2	825	51.5	311	1	O2T1_HUMAN
3	816	50.9	314	1	O2Z1_HUMAN
4	811	50.6	323	1	O2T2_HUMAN
5	804	50.2	315	1	O2T5_HUMAN
6	801	50.0	316	1	O2T8_HUMAN
7	794	49.6	312	1	O2M6_HUMAN
8	793	49.5	320	1	O2AK_HUMAN
9	777	48.5	312	1	O2M7_HUMAN
10	776	48.4	320	1	O2T4_HUMAN
11	749	46.8	313	1	O2T3_HUMAN
12	747.5	46.7	312	1	O2L8_HUMAN
13	733.5	45.8	312	1	O2L2_HUMAN
14	721	45.0	310	1	O2A1_HUMAN
15	713.5	44.5	312	1	O2L8_HUMAN
16	708.5	44.2	312	1	O2L2_HUMAN
17	702	43.8	314	1	O2D3_HUMAN
18	696	43.4	315	1	O2V2_HUMAN
19	695	43.4	315	1	O2V3_HUMAN
20	688	42.9	310	1	O2AC_HUMAN
21	684.5	42.7	323	1	O2AE_HUMAN
22	684	42.7	312	1	O2L1_MOUSE
23	679	42.4	314	1	O2L1_MOUSE
24	678	42.3	312	1	O2H2_HUMAN
25	678	42.3	314	1	O2D1_HUMAN
26	677.5	42.3	316	1	O2H3_HUMAN
27	676	42.2	316	1	O2H3_HUMAN
28	675	42.1	312	1	O2C1_HUMAN
29	674	42.1	313	1	O2G1_PANTR
30	671.5	41.9	309	1	O2G3_HUMAN
31	671	41.9	318	1	O2C2_HUMAN
32	668.5	41.7	313	1	O2H1_HUMAN
33	667	41.6	316	1	O2H1_HUMAN

34	666.5	41.6	319	1	O2S2_HUMAN	O9ngn1 homo sapien
35	666	41.6	311	1	O1N3_HUMAN	O8ngs0 homo sapien
36	664	41.4	317	1	ODC3_HUMAN	O8ngs6 homo sapien
37	663	41.4	317	1	OR14_MOUSE	O8vfk7 mus musculu
38	663	41.4	318	1	ODC4_HUMAN	O8ngs5 homo sapien
39	663	41.4	324	1	OR07_MOUSE	O8vks2 mus musculu
40	662.5	41.4	311	1	O1I6_HUMAN	O8ngt2 homo sapien
41	662	41.3	309	1	O1A1_HUMAN	O9piq5 homo sapien
42	662	41.3	317	1	OLF3_CANFA	O9s156 canis fami
43	661	41.3	309	1	O1A2_HUMAN	O9y585 homo sapien
44	658	41.1	309	1	O1A1_PANTR	O9tuat7 pan troglod
45	658	41.1	321	1	O5V1_HUMAN	O9ugf6 homo sapien

ALIGNMENTS

RESULT 1

ID	O2AG_HUMAN	STANDARD;	PRT;	316 AA.
AC	O9H205; O96R26;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Olfactory receptor 2AG1 (HT3).			
GN	OR2AG1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_Taxid:9606;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RA	Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,			
RA	Tsutsuni S., Aburatani H., Asai K., Akiyama Y.;			
RT	"Genome-wide discovery and analysis of human seven transmembrane helix			
RT	receptor genes.";			
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
RM	[2]			
RP	SEQUENCE OF 68-284 FROM N.A.			
RX	MEDLINE=22202146; PubMed=12213199;			
RA	Fuchs T., Malecova B., Linhart C., Sharan R., Khen M., Herwig R.,			
RA	Shmulevich D., Elkon R., Steinbach M., O'Brien J.K., Radelof U.,			
RT	Lehnach H., Lancel D., Shamir R.;			
RT	"DEPOG: a practical scheme for deciphering families of genes.";			
RL	Genomics 80:295-302(2002).			
RM	[3]			
RP	SEQUENCE OF 152-316 FROM N.A.			
RX	MEDLINE=21310002; PubMed=11416212;			
RA	Lane R.P., Cutforth T., Young J., Athanasiou M., Friedman C.,			
RA	Rowen L., Evans G., Axel R., Hood L., Trask B.J.;			
RT	"Genomic analysis of orthologous mouse and human olfactory receptor			
RT	loci.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 98:7390-7395(2001).			
CC	- FUNCTION: Putative odorant receptor.			
CC	- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.			
CC	- DATABASE: NAME=Human Olfactory Receptor Data Explorer (HOREDE);			
CC	WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HOREDE/showgene.pl?key=symbol&			
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DR	EMBL; AB065823; BAC06042.1; -			
DR	EMBL; AF399618; AAK95103.1; -			
DR	EMBL; AF321237; AAG45209.1; -			
DR	Genew; HGNC:15147; OR2AG1.			
DR	InterPro; IPR00276; GPCR_Rhodpsn.			
DR	Pfam; PF00001; Tcm_1; 1.			


```

QY 246 IVVGMFYGAATFMYVLPSSFSHPKQNIISVFYITVPLNPLIYSLNKEVNRALRYV 305
DB 245 TVVSLFYGAATYMLPHSHYKPAQKVLVSFYTILTPMLNPLIYSLNKEVNRALRYV 304
QY 306 GKX 308
DB 305 GRP 307

RESULT 3
0221 HUMAN STANDARD; PRT; 314 AA.
AC 08NG67; Q96R25; (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Olfactory receptor 22L.
GN OR22L OR OR222.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Putami K., Matsumoto S.,
RA Tautsund S., Aburatani H., Asai K., Akiyama Y.;
RT "Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 68-284 FROM N.A.
RA MEDLINE=2202146; PubMed=12213199;
RA Fuchs T., Malcovova B., Linhart C., Sharan R., Khen M., Herwig R.,
RA Shmulevich D., Elkon R., Steinfath M., O'Brien J.K., Radeflof U.,
RA Lehnach H., Lancel D., Shamir R.;
RT "DEFOG: a practical scheme for deciphering families of genes."
RL Genomics 80:295-302(2002).
CC -!- FUNCTION: Putative odorant receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -!- DATABASE: NAME=Human Olfactory Receptor Data Exploratorium (HORDE);
CC WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&
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CC -----
DR EMBL; AB065930; BAC06145.1; -
DR EMBL; AF399619; AAK95104.1; -
DR Genew; HGNC:15391; OR22L.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1.1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 25
FT TRANSMEM 26 49
FT DOMAIN 50 57
FT TRANSMEM 58 79
FT DOMAIN 100 100
FT TRANSMEM 101 120
FT DOMAIN 121 139
FT TRANSMEM 140 158
FT DOMAIN 159 195
FT TRANSMEM 196 219
FT DOMAIN 220 236

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FT TRANSMEM 237 259
FT DOMAIN 260 272
FT TRANSMEM 273 292
FT DOMAIN 293 314
FT CARBOHYD 5 5
SQ SEQUENCE 314 AA; 34444 MW; 537E389A5EDA471F CRC64;

Query Match
Best Local Similarity 50.8%; Score 816; DB 1; Length 314;
Matches 154; Conservative 55; Mismatches 94; Indels 0; Gaps 0;

QY 5 NSTLGGFIVGILNDSSPELLVATFTLVMLATLSNGLLATITERTALHMPYLLG 64
DB 5 NOSVASDFLVGLFHSRSGRQLLFSLVAFVYIGLVTLFLRVDSRLHMPYELL 64
QY 65 QSLNDLFTSVTPKALADFLRRENTISFGGALOMPLATMGSAEDLLFMAYDRY 124
DB 65 QSLDFDGPMTYTRKMSDFLRGCAATSYGGAAQIFPLTLMGVAEGVLVIMSTDRY 124
QY 125 AICHPKMTLMSPPVCMIVATSWILASLIAGHTMYTHLPFCVSWERHLLCEIPDL 184
DB 125 AVCPLOYVLMRRQVCLLMGSSMWVGLVMSIQTSITLHPYCASRIVDHFCVPL 184
QY 185 LKLACADTSRYELLIVYGVTPLLPISAIYASYTLVFTVLRMPSNEGRKALVTCSH 244
DB 185 LKLSCADTCAYEMALSTSGVLLTLMPLSLIATSYGHVLAVALMSRSEARHRAVTCSSH 244
QY 245 IIVGMFYGAATFMYVLPSSFSHPKQNIISVFYITVPLNPLIYSLNKEVNRALRYV 304
DB 245 IIVGELFYGAATFMYVLPSSFSHPKQNIISVFYITVPLNPLIYSLNKEVNRALRYV 304
QY 305 LCK 307
DB 305 LSR 307

RESULT 4
0272 HUMAN STANDARD; PRT; 323 AA.
AC 08NGX2;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Olfactory receptor 272.
GN OR272.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Putami K., Matsumoto S.,
RA Tautsund S., Aburatani H., Asai K., Akiyama Y.;
RT "Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Putative odorant receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -!- DATABASE: NAME=Human Olfactory Receptor Data Exploratorium (HORDE);
CC WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&
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CC -----
DR EMBL; AB065644; BAC05870.1; -
DR Genew; HGNC:14725; OR272.
DR InterPro; IPR000276; GPCR_Rhodopsn.

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RESULT 6
O2TB_HUMAN
ID O2TB_HUMAN STANDARD; PRT; 316 AA.
AC Q8NH01;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Olfactory receptor 2T11.
GN OR2T11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RX
RN
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Tsubumai S., Aburatani H., Asai K., Akiyama Y.;
RT "Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Putative odorant receptor.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -1- DATABASE: NAME=Human Olfactory Receptor Data Exploratorium (HORDE);
CC WWW="http://bioinformatics.weimann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&
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CC -----
DR EMBL; AB065614; BAC05841.1; -
DR Genew; HGNC:19574; OR2T11.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G PROTEIN RECP F1_1; FALSE_NEG.
DR PROSITE; PS50262; G PROTEIN RECP F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 22 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 23 46 1 (POTENTIAL).
FT DOMAIN 47 54 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 55 76 2 (POTENTIAL).
FT DOMAIN 77 97 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 98 117 3 (POTENTIAL).
FT DOMAIN 118 136 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 137 155 4 (POTENTIAL).
FT DOMAIN 156 192 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 193 216 5 (POTENTIAL).
FT DOMAIN 217 233 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 234 253 6 (POTENTIAL).
FT DOMAIN 257 269 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 270 289 7 (POTENTIAL).
FT DOMAIN 290 316 CYTOPLASMIC (POTENTIAL).
FT DISULFID 94 186 BY SIMILARITY.
FT CARBOHYD 3 3 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 316 AA; 34797 MW; E785C0788F405FD8 CRC64;

Query Match 50.0%; Score 801; DB 1; Length 316;
Best Local Similarity 51.5%; Pred. No. 4,3e-51;
Matches 154; Conservative 54; Mismatches 91; Indels 0; Gaps 0;

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OY 6 STLGSEFIIIVGLINDSGSEELIYATFTIIMALITNSGILLATITEARLHPMYLLSQ 65
DB 3 NTSSSDFTLLGLVNSEAGIVFTVLAVFLGVTNLVWIFLIQVDSRLHPMYLLSQ 62
OY 66 LSLMDLLFTSVTPKALDELRENTISFGGCAQLQELAVLWMSADLLAFAYARYYA 125
DB 63 LSLMDLLFTSVTPKALDELRENTISFGGCAQLQELAVLWMSADLLAFAYARYYA 122

OY 126 ICHPLKMYTMSDRVCWIVATSWILASLAIIGHTNYMHPFCVSMELRHLLCEIPPLL 185
DB 123 VCNPLRYPYLMNRKCKLLLAAGMFGSLDGLFTPTITMNVVPCGSRISINHFCETPAVL 182
OY 186 KLAACATSTSEYELIYTGTFLLPLPSAIVASTTVLFTVLRPNSDEGRKALVTCSHL 245
DB 183 KLAACATSTSEYELIYTGTFLLPLPSAIVASTTVLFTVLRPNSDEGRKALVTCSHL 242
OY 246 IYVGMFYGATFMYVLPSSFSHPKODNIISVFITYTPTALNPLIYSLRNKEVRLRRV 304
DB 243 TVVSTFYGAFFITYVLPSSFSHPKODNIISVFITYTPTALNPLIYSLRNKEVRLRRV 301

RESULT 7
O2M6_HUMAN
ID O2M6_HUMAN STANDARD; PRT; 312 AA.
AC Q8NGS3;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Olfactory receptor 2M6.
GN OR2M6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RX
RN
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Tsubumai S., Aburatani H., Asai K., Akiyama Y.;
RT "Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Putative odorant receptor.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -1- DATABASE: NAME=Human Olfactory Receptor Data Exploratorium (HORDE);
CC WWW="http://bioinformatics.weimann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&
CC -----
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DR EMBL; AB065952; BAC06165.1; -
DR Genew; HGNC:19593; OR2M6.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G PROTEIN RECP F1_1; 1.
DR PROSITE; PS50262; G PROTEIN RECP F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 26 49 1 (POTENTIAL).
FT DOMAIN 50 57 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 58 79 2 (POTENTIAL).
FT DOMAIN 80 100 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 101 120 3 (POTENTIAL).
FT DOMAIN 121 139 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 140 158 4 (POTENTIAL).
FT DOMAIN 159 195 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 196 219 5 (POTENTIAL).
FT DOMAIN 220 236 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 237 259 6 (POTENTIAL).
FT DOMAIN 260 272 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 273 292 7 (POTENTIAL).
FT DISULFID 293 311 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 312 311 BY SIMILARITY.

```

FT CARBOHYD 5 5 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 312 AA; 34827 MW; SCEFA28A1948C2F2 CRC64;
 Query Match 49.5%; Score 794; DB 1; Length 312;
 Best Local Similarity 49.5%; Pred. No. 1,4e-50;
 Matches 152; Conservative 51; Mismatches 104; Indels 0; Gaps 0;

QY 1 MELRNSTLGSGLFVIGLINDSGSPPELLYATPTLLMYMLATNSGLLAIITTEARLHPMY 60
 DB 1 MAENSTFNDSFILLGIFNHSPTHTFFFLVLAIFSFAFNGNSWMLVLLIDQLHPMY 60
 QY 61 LLLGSLMDLFTSVTPPALADFLRENTISFGGALOMFLALINGSAEDLLAMAY 120
 DB 61 LLLSQSLMDLMLCTVPPKAAFNYSLSGSKSISWAGCATQIFPTYSILGSECFLLAMAY 120
 QY 121 DRYVAICHPLKMYTMSPRCWMVATSWILASILAIGHMYTMHLPCVSWELRHLLCE 180
 DB 121 DRYVAICHPLRYNLMSPKICGIMTAFSWILGTDGIIIVAFSFSYCSRETAHFFCD 180
 QY 181 IPELLKLACADTSRYELIIVTGVTFLLPISAVASYTLVLFVLMPSNEGRKALVT 240
 DB 181 FPLSLILSCDSTISFEKILPTCCIVMTVPVAILIASYAVILAVIMSGEGGRKAFIT 240
 QY 241 CSSHLIVGMFYGAATMYVLPSSFHSPKODNITSVYTTVTPLNPLIYSLRKEVMRA 300
 DB 241 CSSHLIVGMFYGAALFMYIRPTSDRSPQDKXWVVFYTLTPMLNPLIYSLRKEVTRA 300
 QY 301 LRRYLK 307
 DB 301 FMKILGK 307

RESULT 8
 02AK_HUMAN
 ID_02AK_HUMAN STANDARD; PRT; 320 AA.
 AC Q8NG81;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Olfactory receptor 2AK2.
 GN OR2AK2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
 RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
 RT "Genome-wide discovery and analysis of human seven transmembrane helix
 RT receptor genes";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Putative odorant receptor.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -1- DATABASE: NMR-Human Olfactory Receptor Data Explorer (HORDE);
 CC WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL; AB065951; BAC06164.1; -
 DR GENM; HGNC:19569; OR2AK2.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCR_RHODOPSIN.
 DR PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECPT_F1_2; 1.

KW G-protein coupled receptor; Transmembrane; glycoprotein;
 FM Multigene family; Olfaction.
 FT DOMAIN 1 25
 FT TRANSEM 26 49
 FT TRANSEM 50 57
 FT DOMAIN 58 79
 FT TRANSEM 80 100
 FT TRANSEM 101 120
 FT DOMAIN 121 139
 FT TRANSEM 140 158
 FT DOMAIN 159 195
 FT TRANSEM 196 219
 FT DOMAIN 220 236
 FT TRANSEM 237 259
 FT DOMAIN 260 272
 FT TRANSEM 273 292
 FT DOMAIN 293 320
 FT DISULFID 97 189
 FT CARBOHYD 5 5
 SQ SEQUENCE 320 AA; 36157 MW; B1354765B15557A CRC64;
 Query Match 49.5%; Score 793; DB 1; Length 320;
 Best Local Similarity 49.5%; Pred. No. 1,6e-50;
 Matches 153; Conservative 45; Mismatches 111; Indels 0; Gaps 0;

QY 1 MELRNSTLGSGLFVIGLINDSGSPPELLYATPTLLMYMLATNSGLLAIITTEARLHPMY 60
 DB 1 MKTGNQSGFGTDFLLVGLFGYGIWINSLLFVYATLFTVALTGIMLILHILIRLTRHPMY 60
 QY 61 LLLGSLMDLFTSVTPPALADFLRENTISFGGALOMFLALINGSAEDLLAMAY 120
 DB 61 FLLSQSLMDLMLCTVPPKAAVFSLSQSKIRIRLGEIQTGYVFLAGGTALLGMSY 120
 QY 121 DRYVAICHPLKMYTMSPRCWMVATSWILASILAIGHMYTMHLPCVSWELRHLLCE 180
 DB 121 DRYVAICHPLHYFMILMSKICCLMVACAWASGINAHTILYVQLFCFSRLINHPCE 180
 QY 181 IPELLKLACADTSRYELIIVTGVTFLLPISAVASYTLVLFVLMPSNEGRKALVT 240
 DB 181 VPALLSLVQDTSQYEVYVLLSGIILLLPFLAIASVAVILVFPQSSGKGAKAVST 240
 QY 241 CSSHLIVGMFYGAATMYVLPSSFHSPKODNITSVYTTVTPLNPLIYSLRKEVMRA 300
 DB 241 CSSHLIVASLFFVATPTFTYRPHSLRSPDKAVAVYTTVTPLNPLIYSLRKEVGA 300
 QY 301 LRRYLK 309
 DB 301 VRLGLTWI 309

RESULT 9
 02M7_HUMAN
 ID_02M7_HUMAN STANDARD; PRT; 312 AA.
 AC Q8NG81;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Olfactory receptor 2M7.
 GN OR2M7.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
 RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
 RT "Genome-wide discovery and analysis of human seven transmembrane helix
 RT receptor genes";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Putative odorant receptor.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

CC -1- DATABASE: NAME=Human Olfactory Receptor Data Exploratorium (HORDE);
 CC WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&
 CC
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DR EMBL: AB065954; BAC06167.1; -
 DR Genew; HGNC:19594; OR247.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCRHOPOPSN.
 DR PROSITE; PS00237; G PROTEIN RECP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Olfaction.

FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 26 49 1 (POTENTIAL).
 FT DOMAIN 50 57 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 58 79 2 (POTENTIAL).
 FT DOMAIN 80 100 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 101 120 3 (POTENTIAL).
 FT DOMAIN 121 139 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 140 158 4 (POTENTIAL).
 FT DOMAIN 159 195 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 196 219 5 (POTENTIAL).
 FT DOMAIN 220 236 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 237 259 6 (POTENTIAL).
 FT DOMAIN 260 272 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 273 292 7 (POTENTIAL).
 FT DOMAIN 293 311 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 97 189 BY SIMILARITY.
 FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 312 AA; 34902 MW; 42A9A1D7EB861E88 CRC64;

Query Match 48.5%; Score 777; DB 1; Length 312;
 Best Local Similarity 48.2%; Pred. No. 2.3e-49;
 Matches 148; Conservative 51; Mismatches 108; Indels 0; Gaps 0;

QY 1 MELNSTLGSGLFVGLINDSGSPDLLVATFTLLMALTSGNLLLAITTEARLHMPY 60
 DB 1 MAMENQFNSDFLLGLIFNHSPTHTPLFVLALFVSVAFMGNSIMVLLIYDTQHTPMY 60
 QY 61 LLLGQSLMDLFTSVTPKRALDFLRRENTISFGGCAOMFLATMGSAEDLLAFMAY 120
 DB 61 FLISQSLMDLMLCTTVPKRAFNYLGSKXISNAGCATQIFFYISLGSCEFLAAVSY 120
 QY 121 DRYVAICHPKMYMTLSPRCVMIVATSWILASILAIGHMYTMHLPFCVSEIRHLICE 180
 DB 121 DRYVAICHPKMYMTLSPRCVMIVATSWILASILAIGHMYTMHLPFCVSEIRHLICE 180
 QY 181 IPPLLKLAADTSRYELIYVTVFLPLISATVASYTLVFLVLRMPSEGRKALVT 240
 DB 181 FPSLLILSNDTSIFEEVIFICCIYMLVFPAIIITTSVAVILAVIHMGSEGRKAFVT 240
 QY 241 CSSHLIYVGMFYGAATPMYVLPSSFHSPKQNTISVFTTYTPALNPLIYLNRKEWRA 300
 DB 241 CSSHLIYVGMFYGAATPMYVLPSSFHSPKQNTISVFTTYTPALNPLIYLNRKEWRA 300
 QY 301 LRRVYLGK 307
 DB 301 LRRVYLGK 307
 QY 301 LRRVYLGK 307
 DB 301 LRRVYLGK 307

RESULT 10
 O2T4 HUMAN STANDARD; PRT; 320 AA.
 AC Q8NH00;
 DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Olfactory receptor 274.
 GN OR24.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
 RA Taniuchi S., Aburatani H., Asai K., Akiyama Y.
 RT "genome-wide discovery and analysis of human seven transmembrane helix
 RT receptor genes.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Putative odorant receptor.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -1- DATABASE: NAME=Human Olfactory Receptor Data Exploratorium (HORDE);
 CC WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&
 CC
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DR EMBL: AB065615; BAC05842.1; -
 DR Genew; HGNC:15016; OR24.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCRHOPOPSN.
 DR PROSITE; PS00237; G PROTEIN RECP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Olfaction.

FT DOMAIN 1 29 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 30 53 1 (POTENTIAL).
 FT DOMAIN 54 61 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 62 83 2 (POTENTIAL).
 FT DOMAIN 84 104 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 105 124 3 (POTENTIAL).
 FT DOMAIN 125 143 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 144 162 4 (POTENTIAL).
 FT DOMAIN 163 199 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 200 223 5 (POTENTIAL).
 FT DOMAIN 224 240 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 241 263 6 (POTENTIAL).
 FT DOMAIN 264 276 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 277 296 7 (POTENTIAL).
 FT DOMAIN 297 320 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 101 193 BY SIMILARITY.
 FT CARBOHYD 3 9 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 9 9 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 190 190 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 320 AA; 36124 MW; 501ECD4B237CF7D CRC64;

Query Match 48.4%; Score 776; DB 1; Length 320;
 Best Local Similarity 50.2%; Pred. No. 2.8e-49;
 Matches 152; Conservative 52; Mismatches 99; Indels 0; Gaps 0;

QY 3 LNSTLGSGLFVGLINDSGSPDLLVATFTLLMALTSGNLLLAITTEARLHMPYLL 62
 DB 7 MAMTGMSPDFLLGLFQSKHPALLCVIVFVPMALSGNVALILLIHCHDAHLTPMYEF 66
 QY 63 LGLSLMDLFTSVTPKRALDFLRRENTISFGGCAOMFLATMGSAEDLLAFMAYDR 122
 DB 67 ISQLSMDMAYISVTPKMLLDQWGVNKSISAPBCGMQPFYVTLASGEFLATMAYDR 126
 QY 123 YVAICHPKMYMTLSPRCVMIVATSWILASILAIGHMYTMHLPFCVSEIRHLICEIP 182

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DR EMBL; AB065627; BAC05853.1; -
DR Genew; HGNC:15014; OR218.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 24
FT TRANSMEM 25 48
FT DOMAIN 49 56
FT TRANSMEM 57 78
FT DOMAIN 79 99
FT TRANSMEM 100 119
FT DOMAIN 120 138
FT TRANSMEM 139 157
FT DOMAIN 158 194
FT TRANSMEM 195 218
FT DOMAIN 219 235
FT TRANSMEM 236 258
FT DOMAIN 259 271
FT TRANSMEM 272 291
FT DOMAIN 292 312
FT DISULFID 96 188
FT CARBOHYD 5 5
FT CARBOHYD 88 88
SQ SEQUENCE 312 AA; 35444 MW; 845325F98685AD4 CRC64;

Query Match 46.7%; Score 747.5; DB 1; Length 312;
Best Local Similarity 47.7%; Pred. No. 3.1e-47;
Matches 145; Conservative 49; Mismatches 109; Indels 1; Gaps 1;

QY 1 MELRNSTLGSGLFVGIINDSGSPPELLYATFTILYMLALTSNGLLLAATTEARLHPMY 60
DB 1 MERNVNT-STDFLLDGLFPSPRIDLFFLLIVFTFMALIGLMSMLLFLDTHATPMY 59
QY 61 LLLGQSLNDLFTSVVTPKALDFLRRENTISFGGALOMFLATMGSAEDLLAFMAY 120
DB 60 FILSQSLIDLVYISITVPRKASDFLHGKKSISFTGCGISQFFPLALGAEALLASMAV 119
QY 121 DRYVAICHLKMTLMSPRVCIMVATSWILASLAIHGTWYTHLPFCVSWEIRHLCE 180
DB 120 DRYVAICFLHYLIRMSKVCVIMTIGSWIGSINACHTVYVLIHPCRSRAINHFCD 179
QY 181 IPELKLACADTSRYELIIVGVFPLLPISAIYASYLVLPYLARMSNGRKAAYT 240
DB 180 VPAAMTTLACMDTWYEGVLFSAITFLVPPFGISCSYQVLFAYHMSAGRKAAYT 239
QY 241 CSHHIVGMFYGAATFMYLPPSPKODNIISVFTYIVPALNPLIYSIRKXVMA 300
DB 240 CSTHLTVVTFYAFPYVTLRPRSLRSPEDKLVAVFYIILPMLNPIIYSIRKXVMA 299
QY 301 LRRV 304
DB 300 LTRV 303

RESULT 13
0212_HUMAN STANDARD; PRT; 312 AA.
AC Q8NHI6;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Olfactory receptor 212 (HPRCH07).
GN OR212.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Putani K., Matsumoto S.,
RA Teutani S., Aburatani H., Asai K., Akiyama Y.;
RA "Genome-wide discovery and analysis of human seven transmembrane helix
RA receptor genes.";
RN Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
RP [2]
RP SEQUENCE OF 125-238 FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=92131132; PubMed=1370853;
RA Parmentier M., Llobet P., Schurians S., Schiffmann S., Jelfort A.,
RA Eggerickx D., Ledent C., Mollereau C., Gerard C., Perret J.,
RA Grootegeed A., Vassart G.;
RT "Expression of members of the putative olfactory receptor gene family
RT in mammalian germ cells.";
RL Nature 355:453-455(1992).
CC -!- FUNCTION: Putative odorant receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -!- DATABASE: NAME=Human Olfactory Receptor Data Explorerium (HORDE);
CC WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showgene.pl?key=symbol&
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DR EMBL; AB065597; BAC05825.1; -
DR EMBL; X64978; -; NOT ANNOTATED_CDS.
DR Genew; HGNC:8266; OR212.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 24
FT TRANSMEM 25 48
FT DOMAIN 49 56
FT TRANSMEM 57 78
FT DOMAIN 79 99
FT TRANSMEM 100 119
FT DOMAIN 120 138
FT TRANSMEM 139 157
FT DOMAIN 158 194
FT TRANSMEM 195 218
FT TRANSMEM 219 235
FT TRANSMEM 236 258
FT DOMAIN 259 271
FT TRANSMEM 272 291
FT DISULFID 96 188
FT CARBOHYD 5 5
FT CARBOHYD 88 88
SQ SEQUENCE 312 AA; 35495 MW; C85F0368D85CIDE CRC64;

Query Match 45.8%; Score 733.5; DB 1; Length 312;
Best Local Similarity 47.2%; Pred. No. 3.2e-46;
Matches 145; Conservative 52; Mismatches 109; Indels 1; Gaps 1;

QY 1 MELRNSTLGSGLFVGIINDSGSPPELLYATFTILYMLALTSNGLLLAATTEARLHPMY 60


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CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -1- DATABASE: NAME=Human Olfactory Receptor Data Exploratorium (HORDE);
CC WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&
CC -----
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CC -----
DR EMBL; AB065956; BAC06169.1; -.
DR Genew; HGNC:19570; OR2L11.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1.
DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2_1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 24 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 25 48 1 (POTENTIAL).
FT DOMAIN 49 56 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 57 78 2 (POTENTIAL).
FT DOMAIN 79 99 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 100 119 3 (POTENTIAL).
FT DOMAIN 120 138 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 139 157 4 (POTENTIAL).
FT DOMAIN 158 194 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 195 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 258 6 (POTENTIAL).
FT DOMAIN 259 271 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 272 291 7 (POTENTIAL).
FT DOMAIN 292 312 CYTOPLASMIC (POTENTIAL).
FT DISULFID 96 188 BY SIMILARITY.
FT CARBOHYD 5 5 N-LINKED (GICNAC. . .) (POTENTIAL).
SQ SEQUENCE 312 AA; 35648 MW; E04FEB75A902863 CRC64;

Query Match 44.5%; Score 713.5; DB 1; Length 312;
Best Local Similarity 46.2%; Pred. No. 8.8e-45;
Matches 141; Conservative 50; Mismatches 113; Indels 1; Gaps 1;

QY 1 MEIRNSTIGSGFIIYGLINDSGPELLATFTILYMLATNSGLLATITIEARLMPY 60
DB 1 MENYQT-STDFILGLPPSKIGLFLFTILFVILFIMALIGNLSMILIFLDTHLTPY 59
QY 61 ILLGQLSMDLLEFVSVPKALADFLRENTISFGCALQWFLALTMGSAEDLLAFMY 120
DB 60 FLISQLSLIDLNYISTIVPKASDPLYGKKSISFICGQISFFMTFAGAEALLLTSMAY 119
QY 121 DRYVAICHPLKMYTMSPRVCWIVATSWILASLIAIGHTYTMHLPCVSWIEIRHLCE 180
DB 120 DRYVAICFPLHPYIRMSKRMVLMITGSMIGSINSCAHYARIPYCKSRAINHFCD 179
QY 181 IPPLLAKACADTSRELLIYTGVTPLLPISAIYASTVLVFTVLRMPDSNEGRKALVT 240
DB 180 VPAMLTTLACTDTWYEVFLSTIFLVFPFGIACSYGWLAVYRMHSAEGRKAYST 239
QY 241 CSSHLIVGMFGATFMVLPSSFSHPKODIISVFYTIYPRANPLIYSIRKENVRA 300
DB 240 CSTHLIVTTFYIAPAYTTLCPRSRLSLTEKVLAVFYTILPMLNPIIYSIRKENVGA 299
QY 301 LRRVYL 305
DB 300 LTRVYL 304
```

Search completed: August 18, 2004, 08:57:07
Job time : 14 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2004, 08:36:58 ; Search time 78 Seconds

(without alignments)
1278.253 Million cell updates/sec

Title: US-10-024-444B-2

Sequence: 1 MELNSTLGGSGFLVGIIND.....VMRLARVLGKYLILASTL 316

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SPREMBL_25:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1324	82.6	316	11 Q9EPF8	Q9EPF8 mus musculu
2	1312	81.9	316	11 Q9D3U9	Q9D3U9 mus musculu
3	1308	81.6	316	11 Q8VGT0	Q8VGT0 mus musculu
4	1308	81.6	316	11 Q9D4F9	Q9D4F9 mus musculu
5	1305	81.5	316	11 Q7TRN2	Q7TRN2 mus musculu
6	1304	81.4	316	11 Q9EPF7	Q9EPF7 mus musculu
7	1276	79.7	316	11 Q8VEM5	Q8VEM5 mus musculu
8	1248	77.9	316	11 Q9EPF5	Q9EPF5 mus musculu
9	1243	77.6	315	11 Q8VFP8	Q8VFP8 mus musculu
10	1236	77.2	311	11 Q7TRN4	Q7TRN4 mus musculu
11	1230	76.8	311	11 Q8VEM6	Q8VEM6 mus musculu
12	1210.5	75.6	315	11 Q8VEM3	Q8VEM3 mus musculu
13	1205	75.2	316	11 Q8VEM3	Q8VEM3 mus musculu
14	1204	75.2	317	11 Q8VEM4	Q8VEM4 mus musculu
15	1203	75.1	315	11 Q9EPF6	Q9EPF6 mus musculu
16	1178	73.5	316	11 Q7TRN3	Q7TRN3 mus musculu

17	846	52.8	317	11 Q8VGD7	Q8VGD7 mus musculu
18	839	52.4	314	11 Q7TRX2	Q7TRX2 mus musculu
19	836	52.2	315	11 Q8VGD8	Q8VGD8 mus musculu
20	836	52.2	317	11 Q8VGT5	Q8VGT5 mus musculu
21	833	52.0	317	4 Q8NH04	Q8NH04 homo sapien
22	824	51.4	314	11 Q7TRX1	Q7TRX1 mus musculu
23	822	51.3	308	11 Q8VFG8	Q8VFG8 mus musculu
24	816	50.9	320	11 Q7TRZ2	Q7TRZ2 mus musculu
25	811	50.6	323	4 Q8NGX2	Q8NGX2 mus musculu
26	809.5	50.5	335	11 Q7TRX7	Q7TRX7 mus musculu
27	808	50.4	312	11 Q7TRX0	Q7TRX0 mus musculu
28	806	50.3	314	11 Q7TRX8	Q7TRX8 mus musculu
29	801	50.3	316	4 Q8NH01	Q8NH01 homo sapien
30	800	49.9	310	11 Q7TRZ1	Q7TRZ1 mus musculu
31	798	49.8	310	11 Q8VPD6	Q8VPD6 mus musculu
32	795	49.6	309	11 Q7TRX9	Q7TRX9 mus musculu
33	795	49.6	315	11 Q8VGD9	Q8VGD9 mus musculu
34	794	49.6	312	4 Q8NG83	Q8NG83 mus musculu
35	793	49.5	320	4 Q8NG84	Q8NG84 mus musculu
36	785	49.0	313	11 Q7TS53	Q7TS53 mus musculu
37	780	48.7	313	11 Q7TS51	Q7TS51 mus musculu
38	779	48.6	314	11 Q8VGL7	Q8VGL7 mus musculu
39	777	48.5	312	4 Q8NG81	Q8NG81 homo sapien
40	771.5	48.2	312	11 Q7TS52	Q7TS52 mus musculu
41	771.5	48.2	313	11 Q8VGL6	Q8VGL6 mus musculu
42	771	48.1	306	11 Q7TRZ6	Q7TRZ6 mus musculu
43	771	48.1	306	11 Q7TRZ4	Q7TRZ4 mus musculu
44	770	48.1	312	4 Q8NG29	Q8NG29 homo sapien
45	767	47.9	316	11 Q8VFX7	Q8VFX7 mus musculu

ALIGNMENTS

RESULT 1

Q9EPF8 PRELIMINARY; PRT; 316 AA.

AC Q9EPF8; 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)
DE T1 olfactory receptor (Olfactory receptor MOR283-11) (Olfactory receptor GA_x6K02T2PB39-9271198-9270248).
GN GA_x6K02T2PB39-9271198-9270248.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=21310002; PubMed=11616212;
RA Lane R.P., Cutforth T., Young J., Athanasiou M., Friedman C., Rowen L., Evans G., Axel R., Hood L., Trask B.J.;
RT "Genomic analysis of orthologous mouse and human olfactory receptor loci."
RL Proc. Natl. Acad. Sci. U.S.A. 98:7390-7395(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Zhang X., Firestein S.J.;
RT "The olfactory receptor gene superfamily of the mouse."
RL Nat. Neurosci. 0:0-0(2002).
RN [3]
RP SEQUENCE FROM N.A.
RA Adams M.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Young J.M., Shykind B.M., Lane R.P., Tonnes-Priiddy L., Ross J.A., Walker M., Williams E.M., Axel R., Trask B.J.;
RT "Odorant receptor ESTs demonstrate olfactory expression of over 400 genes, extensive alternate splicing, and unequal expression levels."
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

RN [5]
 RP SEQUENCE FROM N.A.
 RA Sanders K.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AR321234; ANG45195.1; -
 DR EMBL; AY073740; AAL61403.1; -
 DR EMBL; AY17827; AAP71171.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1, 1.
 DR PRINTS; PR00237; GPCRHOOPS.
 DR PROSITE; PS50262; G_PROTEIN_RECIP_F1_2; 1.
 KM Receptor.
 SQ SEQUENCE 316 AA; 34981 MW; 5D89HPIBEH17D480 CRC64;
 Query Match 82.6%; Score 1324; DB 11; Length 316;
 Best Local Similarity 82.3%; Pred. No. 6e-110;
 Matches 260; Conservative 23; Mismatches 33; Indels 0; Gaps 0;
 QY 1 MELNSTLGGSGFLIVGILNDGSPPELLYATFTIYMLATSGLLIATITTEARLEMPY 60
 DB 1 MELNSTLGGSGFLIVGILNDGSPPELLYATFTIYMLATSGLLIATITTEARLEMPY 60
 QY 61 LILGQLSLMDLFTSVVTPKALADFLRENTISFGGCAQMFALMTGSAEDLLAFMAY 120
 DB 61 LILGQLSLMDLFTSVVTPKALADFLRENTISFGGCAQMFALMTGSAEDLLAFMAY 120
 QY 61 LILGQLSLMDLFTSVVTPKALADFLRENTISFGGCAQMFALMTGSAEDLLAFMAY 120
 DB 61 LILGQLSLMDLFTSVVTPKALADFLRENTISFGGCAQMFALMTGSAEDLLAFMAY 120
 QY 121 DRYVALCHPLKMTLSPVCMWVATSWILASILAIGHYTMHLPCVSWETRIHLICE 180
 DB 121 DRYVALCHPLKMTLSPVCMWVATSWILASILAIGHYTMHLPCVSWETRIHLICE 180
 QY 121 DRYVALCHPLKMTLSPVCMWVATSWILASILAIGHYTMHLPCVSWETRIHLICE 180
 DB 121 DRYVALCHPLKMTLSPVCMWVATSWILASILAIGHYTMHLPCVSWETRIHLICE 180
 QY 181 IPLPLKACADTSRYELIYVTVGTFLLPLISAIVASYTLVLFYLRMPSNEGRKKALVT 240
 DB 181 IPLPLKACADTSRYELIYVTVGTFLLPLISAIVASYTLVLFYLRMPSNEGRKKALVT 240
 QY 241 CSSHLIVGMFGAATFMYVLPSSFSHPKODNIISVFYITVPALNPLIYSLRKEVIGA 300
 DB 241 CSSHLIVGMFGAATFMYVLPSSFSHPKODNIISVFYITVPALNPLIYSLRKEVIGA 300
 QY 241 CSSHLIVGMFGAATFMYVLPSSFSHPKODNIISVFYITVPALNPLIYSLRKEVIGA 300
 DB 241 CSSHLIVGMFGAATFMYVLPSSFSHPKODNIISVFYITVPALNPLIYSLRKEVIGA 300
 QY 301 LRRVLGKYTLIAHSTL 316
 DB 301 LRRVLGKYTLIAHSTL 316
 QY 301 LRRVLGKYTLIAHSTL 316
 DB 301 LRRVLGKYTLIAHSTL 316
 RESULT 2
 Q9D3U9 PRELIMINARY; PRT; 316 AA.
 ID Q9D3U9
 AC 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE 4933433602rik protein (Olfactory receptor MOR283-1) (Olfactory receptor GA_x6K0272PB09-9195805-9196785)
 GN 4933433602RIK OR GA_X6K0272PB09-9195805-9196785.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai U., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hata A., Fukunishi Y., Kono H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml U.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaudo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gardoloi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L., Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S., Hayashizaki Y.;
 RA "functional annotation of a full-length mouse cDNA collection.";
 RT Nature 409:685-690(2001).
 RL
 RP SEQUENCE FROM N.A.
 RA Zhang X., Firestein S.J.;
 RT "The olfactory receptor gene superfamily of the mouse.";
 RL Nat. Neurosci. 0:0-0(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Adams M.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Young J.M., Shykina B.M., Lane R.P., Tomes-Pridy L., Ross J.A., Walker M., Williams E.M., Axel R., Trask B.J.;
 RT "Odorant receptor ESTs demonstrate olfactory expression of over 400 genes, extensive alternate splicing, and unequal expression levels.";
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Sanders K.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK017036; BAB30564.1; -
 DR EMBL; AY073025; AAL60688.1; -
 DR EMBL; AY17822; AAP71166.1; -
 DR MGI; MGI:1914036; 4933433602rik.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1, 1.
 DR PRINTS; PR00237; GPCRHOOPS.
 DR PROSITE; PS50262; G_PROTEIN_RECIP_F1_2; 1.
 KM Receptor.
 SQ SEQUENCE 316 AA; 34916 MW; C2C538B675D3225 CRC64;
 Query Match 81.9%; Score 1312; DB 11; Length 316;
 Best Local Similarity 80.4%; Pred. No. 7e-109;
 Matches 254; Conservative 29; Mismatches 33; Indels 0; Gaps 0;
 QY 1 MELNSTLGGSGFLIVGILNDGSPPELLYATFTIYMLATSGLLIATITTEARLEMPY 60
 DB 1 MELNSTLGGSGFLIVGILNDGSPPELLYATFTIYMLATSGLLIATITTEARLEMPY 60
 QY 61 LILGQLSLMDLFTSVVTPKALADFLRENTISFGGCAQMFALMTGSAEDLLAFMAY 120
 DB 61 LILGQLSLMDLFTSVVTPKALADFLRENTISFGGCAQMFALMTGSAEDLLAFMAY 120
 QY 61 LILGQLSLMDLFTSVVTPKALADFLRENTISFGGCAQMFALMTGSAEDLLAFMAY 120
 DB 61 LILGQLSLMDLFTSVVTPKALADFLRENTISFGGCAQMFALMTGSAEDLLAFMAY 120
 QY 121 DRYVALCHPLKMTLSPVCMWVATSWILASILAIGHYTMHLPCVSWETRIHLICE 180
 DB 121 DRYVALCHPLKMTLSPVCMWVATSWILASILAIGHYTMHLPCVSWETRIHLICE 180
 QY 121 DRYVALCHPLKMTLSPVCMWVATSWILASILAIGHYTMHLPCVSWETRIHLICE 180
 DB 121 DRYVALCHPLKMTLSPVCMWVATSWILASILAIGHYTMHLPCVSWETRIHLICE 180
 QY 241 CSSHLIVGMFGAATFMYVLPSSFSHPKODNIISVFYITVPALNPLIYSLRKEVIGA 300
 DB 241 CSSHLIVGMFGAATFMYVLPSSFSHPKODNIISVFYITVPALNPLIYSLRKEVIGA 300
 QY 241 CSSHLIVGMFGAATFMYVLPSSFSHPKODNIISVFYITVPALNPLIYSLRKEVIGA 300
 DB 241 CSSHLIVGMFGAATFMYVLPSSFSHPKODNIISVFYITVPALNPLIYSLRKEVIGA 300
 QY 301 LRRVLGKYTLIAHSTL 316
 DB 301 LRRVLGKYTLIAHSTL 316
 QY 301 LRRVLGKYTLIAHSTL 316
 DB 301 LRRVLGKYTLIAHSTL 316

Db 301 VRRVGRHILPAHATV 316

RESULT 3

OCV8GU0 PRELIMINARY; PRT; 316 AA.

AC O8VGU0;

DT 01-MAR-2002 (TREMBlrel. 20, Created)

DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE Olfactory receptor MOR283-2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Zhang X., Firestein S.J.;

RT "The olfactory receptor gene superfamily of the mouse.";

RL Nat. Neurosci. 0:0-0(2002).

RN [2]

RP SEQUENCE FROM N.A.

RA Adams M.;

RU Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY073056; AAL60719.1; -

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.

DR InterPro; IPR000276; GPCR_Rhodopsn.

DR Pfam; PF00001; 7tm.1; 1.

DR PRINTS; PR00237; GPCRHHODOPSN.

DR PROSITE; PS50262; G_PROTEIN_RECPR_F1_2; 1.

DR KMW Receptor.

SQ SEQUENCE 316 AA; 35239 MW; 2E05EB6642A34C6 CRC64;

Query Match 81.6%; Score 1308; DB 11; Length 316;

Best Local Similarity 80.4%; Pred. No. 1.6e-108;

Matches 254; Conservative 29; Mismatches 33; Indels 0; Gaps 0;

QY 1 MELRNSTLGGFIVGILNDGSPPELLVATFTILYMLATNSGLLATITTEARLHPMY 60

DB 1 MEPMNSTLGGFIVGILNDGSPPELLCATFTALYMLALISNGLLIVITMDARLHPMY 60

QY 61 LILGQSLMDLFTSVTPKALADFLRRENTISFGGCAIQMFALTMGSAEDLLAFMY 120

DB 61 FLTGQSLMDLFTSVTPKALADFLRRENTISFGGCAIQMFALTMGSAEDLLAFMY 120

QY 121 DRYVAICHPDKMTLMSPRVCMVATSWILASLAIAGHTMYTMHLPCVSWEIRLICE 180

DB 121 DRYVAICHPDKMTLMSPRVCMVATSWILASLAIAGHTMYTMHLPCVSWEIRLICE 180

QY 181 IPPLLKACADTSRYELIYVGVTELLPISAVASYTLVFTYLRMSNGRKKALVT 240

DB 181 IPPLLKACADTSRYELIYVGVTELLPISAVASYTLVFTYLRMSNGRKKALVT 240

QY 241 CSSHLIVGMFYGATFMVLPSSFSHPKQDNIIISVFTIYVPALNPLIYSLRNKEVMA 300

DB 241 CSSHLIVGMFYGATFMVLPSSFSHPKQDNIIISVFTIYVPALNPLIYSLRNKEVMA 300

QY 301 LRRVLGKYLIAHSTL 316

DB 301 LRRVLGKYLIAHSTL 316

RESULT 4

Q9D4F9 PRELIMINARY; PRT; 316 AA.

AC Q9D4F9;

DT 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE 4932441H2IRik protein.

GN 4933433E02RIK OR 4932441H2IRIK.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA STRAIN=C57BL/6J; TISSUE=Testis;

RA MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Iawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batzloff S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesele G., Quackenbush J., Schirml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Guelincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli U., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L., Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S., Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

DR EMBL; AK016560; BAB30304.1; -

DR MCD; MG1:1914036; 4933433E02RIK.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.

DR InterPro; IPR000276; GPCR_Rhodopsn.

DR Pfam; PF00001; 7tm.1; 1.

DR PRINTS; PR00237; GPCRHHODOPSN.

DR PROSITE; PS50262; G_PROTEIN_RECPR_F1_2; 1.

SQ SEQUENCE 316 AA; 34930 MW; 231E85FA8BCD207BA CRC64;

Query Match 81.6%; Score 1308; DB 11; Length 316;

Best Local Similarity 80.1%; Pred. No. 1.6e-108;

Matches 253; Conservative 30; Mismatches 33; Indels 0; Gaps 0;

QY 1 MELRNSTLGGFIVGILNDGSPPELLVATFTILYMLATNSGLLATITTEARLHPMY 60

DB 1 MEPMNSTLGGFIVGILNDGSPPELLCATFTALYMLALISNGLLIVITMDARLHPMY 60

QY 61 LILGQSLMDLFTSVTPKALADFLRRENTISFGGCAIQMFALTMGSAEDLLAFMY 120

DB 61 ILRLQSLMDLFTSVTPKALADFLRRENTISFGGCAIQMFALTMGSAEDLLAFMY 120

QY 121 DRYVAICHPDKMTLMSPRVCMVATSWILASLAIAGHTMYTMHLPCVSWEIRLICE 180

DB 121 DRYVAICHPDKMTLMSPRVCMVATSWILASLAIAGHTMYTMHLPCVSWEIRLICE 180

QY 181 IPPLLKACADTSRYELIYVGVTELLPISAVASYTLVFTYLRMSNGRKKALVT 240

DB 181 VPPLLKACADTSRYELIYVGVTELLPISAVASYTLVFTYLRMSNGRKKALVT 240

QY 241 CSSHLIVGMFYGATFMVLPSSFSHPKQDNIIISVFTIYVPALNPLIYSLRNKEVMA 300

DB 241 CSSHLIVGMFYGATFMVLPSSFSHPKQDNIIISVFTIYVPALNPLIYSLRNKEVMA 300

QY 301 LRRVLGKYLIAHSTL 316

DB 301 LRRVLGKYLIAHSTL 316

RESULT 5

Q7TRN2 PRELIMINARY; PRT; 316 AA.

AC Q7TRN2;

DT 07TRN2

01-OCT-2003 (Tremblrel. 25, Created)
 01-OCT-2003 (Tremblrel. 25, Last sequence update)
 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 Olfactory receptor GA_x6K02T2PBj9-9255348-9255398.
 GA_x6K02T2PBj9-9255348-9255398.
 Mus musculus (Mouse).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 NCBI_TaxId=10090;
 [1]
 SEQUENCE FROM N.A.
 Young J.M., Shykind B.M., Lane R.P., Tomes-Priddy L., Rose J.A.,
 Walker M., Williams E.M., Axel R., Trask B.J.;
 "Odorant receptor Esrs demonstrate olfactory expression of over 400
 genes, extensive alternate splicing, and unequal expression levels";
 Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 [2]
 SEQUENCE FROM N.A.
 Senders K.;
 Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AY317826; AAP71170.1; -.
 KM Receptor.
 SQ SEQUENCE 316 AA; 35266 MW; 6318EB6643EB21D CRC64;
 Query Match 81.5%; Score 1305; DB 11; Length 316;
 Best Local Similarity 80.1%; Pred. No. 3e-108;
 Matches 253; Conservative 30; Mismatches 33; Indels 0; Gaps 0;
 QY 1 MELNSTGSGFTLVGILNDGSPPELLYATFTLLYMLATLSNGLLATITEARLHPMY 60
 1 MEPNSTLTGDFNLVGLDSDGSPPELLCATFTALYMLATLSNGLLATITMDARLHPMY 60
 DB 1 LIPPLKACADTSRYELIYVGTGFTLLPISAIIVASYTLVFTVLRMPNSNEGRKALVT 240
 QY 61 LILGQSLMDLFTSVTPKALADFLRENTISFGGCAQMPFALTGSAEDLLATMAY 120
 DB 61 FILGQSLMDLFTSVTPKAVIDFLRDNTISFGGSLQMPFALTGSAEDLLATMAY 120
 QY 121 DRYAICHPLKMTLSPRCVMTWATSWLASLAIHNTYTMHLPCVSWETRIHLCE 180
 DB 121 DRYAICHPLNMYTMRPSICMLVATSWLASLALAGYTTTQYSCSKRIHLCE 180
 QY 181 IPPLKACADTSRYELIYVGTGFTLLPISAIIVASYTLVFTVLRMPNSNEGRKALVT 240
 DB 181 IPPLKACADTSRYELIYVGTGFTLLPISAIIVASYTLVFTVLRMPNSNEGRKALVT 240
 QY 241 CSSHLIVGMFYGATFMVLPSSFSHPKODNIIISVFTYITPALNPLIYSLRKEVRA 300
 DB 241 CSSHLIVGMFYGATFMVLPSSFSHPKODNIIISVFTYITPALNPLIYSLRKEVRA 300
 QY 301 LRRVIGKTYILAHSTL 316
 DB 301 LRRVIGKTYILAHSTL 316
 DB 301 LIRVIGRYIVPAHPTL 316
 RESULT 6
 Q9EPF7 PRELIMINARY; PRT; 316 AA.
 ID Q9EPF7;
 AC 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
 DE T2 olfactory receptor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 STRAIN=C57BL/6J;
 MEDLINE=21310002; PubMed=11416212;
 RA Lane R.P., Outforth T., Young J., Athanasios M., Friedman C.,
 Rowen L., Evans G., Axel R., Hood L., Trask B.J.;
 RT "Genomic analysis of orthologous mouse and human olfactory receptor
 loci";

RL Proc. Natl. Acad. Sci. U.S.A. 98:7390-7395(2001).
 DR EMBL; AF321234; AAG45196.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_Rhodopsin.
 DR PROSITE; PS50262; G_PROTEIN_RECPT_P1_2; 1.
 KM Receptor.
 SQ SEQUENCE 316 AA; 35252 MW; B5029F55D161A1E CRC64;
 Query Match 81.4%; Score 1304; DB 11; Length 316;
 Best Local Similarity 79.7%; Pred. No. 3.6e-108;
 Matches 252; Conservative 31; Mismatches 33; Indels 0; Gaps 0;
 QY 1 MELNSTGSGFTLVGILNDGSPPELLYATFTLLYMLATLSNGLLATITEARLHPMY 60
 1 MEPNSTLTGDFNLVGLDSDGSPPELLCATFTALYMLATLSNGLLATITMDARLHPMY 60
 DB 1 LIPPLKACADTSRYELIYVGTGFTLLPISAIIVASYTLVFTVLRMPNSNEGRKALVT 240
 QY 61 LILGQSLMDLFTSVTPKALADFLRENTISFGGCAQMPFALTGSAEDLLATMAY 120
 DB 61 FILGQSLMDLFTSVTPKAVIDFLRDNTISFGGSLQMPFALTGSAEDLLATMAY 120
 QY 121 DRYAICHPLKMTLSPRCVMTWATSWLASLAIHNTYTMHLPCVSWETRIHLCE 180
 DB 121 DRYAICHPLNMYTMRPSICMLVATSWLASLALAGYTTTQYSCSKRIHLCE 180
 QY 181 IPPLKACADTSRYELIYVGTGFTLLPISAIIVASYTLVFTVLRMPNSNEGRKALVT 240
 DB 181 IPPLKACADTSRYELIYVGTGFTLLPISAIIVASYTLVFTVLRMPNSNEGRKALVT 240
 QY 241 CSSHLIVGMFYGATFMVLPSSFSHPKODNIIISVFTYITPALNPLIYSLRKEVRA 300
 DB 241 CSSHLIVGMFYGATFMVLPSSFSHPKODNIIISVFTYITPALNPLIYSLRKEVRA 300
 QY 301 LRRVIGKTYILAHSTL 316
 DB 301 LRRVIGKTYILAHSTL 316
 DB 301 LIRVIGRYIVPAHPTL 316
 RESULT 7
 Q9EFMS PRELIMINARY; PRT; 316 AA.
 ID Q9EFMS;
 AC 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Olfactory receptor MOR283-4 (Olfactory receptor
 DE GA_x6K02T2PBj9-9184187-9184237).
 GN GA_x6K02T2PBj9-9184187-9184237.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 Zhang X., Firestein S.J.;
 RT "The olfactory receptor gene superfamily of the mouse";
 Nat. Neurosci. 0:0-0(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 Adams M.;
 Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 Young J.M., Shykind B.M., Lane R.P., Tomes-Priddy L., Rose J.A.,
 Walker M., Williams E.M., Axel R., Trask B.J.;
 RT "Odorant receptor Esrs demonstrate olfactory expression of over 400
 genes, extensive alternate splicing, and unequal expression levels";
 Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]

```

RP SEQUENCE FROM N.A.
RA Sanders K.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY073497; AAL61160.1; -.
DR EMBL; AY317821; AAP71165.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS50262; G_PROTEIN_RECEPT_F1_2; 1.
KM Receptor.
SQ SEQUENCE 316 AA; 35283 MW; 3D944A8FA1A7436 CRC64;

Query Match 79.7%; Score 1276; DB 11; Length 316;
Best Local Similarity 78.1%; Pred. No. 1,1e-105;
Matches 246; Conservative 31; Mismatches 38; Indels 0; Gaps 0;

QY 1 MELNSTLGSGLVGLINDSGPELLYATFTLLYMLALNSGLLALITTEARLHPMY 60
DB 1 MELNSTLGSGLVGLINDSGPELLYATFTLLYMLALNSGLLALITTEARLHPMY 60
QY 61 LLLGQSLMDLFTSVTPKRALDFLRRENTISFGCALOMFLATMGSAEDLLAFMAY 120
DB 61 LLLGQSLMDLFTSVTPKRALDFLRRENTISFGCALOMFLATMGSAEDLLAFMAY 120
QY 121 DRYVALCHPLKNTMTSPRCVIMVATSWILASILAIGHMTYTMHLPCVSWERHLLCE 180
DB 121 GRYVALCHPLNTMTSPRCVIMVATSWILASILAIGHMTYTMHLPCVSWERHLLCE 180
QY 181 IPELKLKACADTSREYELIYVGTFTLLPISAIYASYTLVFTVLRMSNEGRKALVT 240
DB 181 IPELKLKACADTSREYELIYVGTFTLLPISAIYASYTLVFTVLRMSNEGRKALVT 240
QY 241 CSNHLIVGMFYGAATFMVLPSSFSHPKODNIISVFTYITVPALNPLIYSLRNKEVMA 300
DB 241 CSNHLIVGMFYGAATFMVLPSSFSHPKODNIISVFTYITVPALNPLIYSLRNKEVMA 300
QY 301 LRRVIGKYLILAHST 315
DB 301 LRRVIGKYLILAHST 315
DB 301 LRRVIGKYLILAHST 315

RESULT 8
Q9EPF5 PRELIMINARY; PRT; 319 AA.
AC Q9EPF5;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE T4 olfactory receptor (Olfactory receptor MOR283-7) (Olfactory
receptor GA_x6K0212PBj9-9222217-9223176).
GN GA_x6K0212PBj9-9222217-9223176.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J;
RX MEDLINE=21310002; PubMed=11416212;
RA Lane R.P., Outforth T., Young J., Athanasiou M., Friedman C.,
RA Rowen L., Evans G., Axel R., Hood L., Trask B.J.;
RT Genomic analysis of orthologous mouse and human olfactory receptor
RT loci."
RL Proc. Natl. Acad. Sci. U.S.A. 98:7390-7395(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Zhang X., Firestein S.J.;
RT "The olfactory receptor gene superfamily of the mouse.";
RL Nat. Neurosci. 0:0-0(2002).

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RP [3]
RP SEQUENCE FROM N.A.
RA Adams M.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
RA Walker M., Williams E.M., Axel R., Trask B.J.;
RT "Odorant receptor B6TS demonstrate olfactory expression of over 400
RT genes, extensive alternate splicing, and unequal expression levels.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Sanders K.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF321234; AAG45198.1; -.
DR EMBL; AY073501; AAL61164.1; -.
DR EMBL; AY317824; AAP71168.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS50262; G_PROTEIN_RECEPT_F1_2; 1.
KM Receptor.
SQ SEQUENCE 319 AA; 35493 MW; 8CFB7ECTA5BDD3D8 CRC64;

Query Match 77.3%; Score 1248; DB 11; Length 319;
Best Local Similarity 75.4%; Pred. No. 3.6e-103;
Matches 236; Conservative 37; Mismatches 40; Indels 0; Gaps 0;

QY 1 MELNSTLGSGLVGLINDSGPELLYATFTLLYMLALNSGLLALITTEARLHPMY 60
DB 1 MELNSTLGSGLVGLINDSGPELLYATFTLLYMLALNSGLLALITTEARLHPMY 60
QY 61 LLLGQSLMDLFTSVTPKRALDFLRRENTISFGCALOMFLATMGSAEDLLAFMAY 120
DB 61 LLLGQSLMDLFTSVTPKRALDFLRRENTISFGCALOMFLATMGSAEDLLAFMAY 120
QY 121 DRYVALCHPLKNTMTSPRCVIMVATSWILASILAIGHMTYTMHLPCVSWERHLLCE 180
DB 121 GRYVALCHPLNTMTSPRCVIMVATSWILASILAIGHMTYTMHLPCVSWERHLLCE 180
QY 181 IPELKLKACADTSREYELIYVGTFTLLPISAIYASYTLVFTVLRMSNEGRKALVT 240
DB 181 IPELKLKACADTSREYELIYVGTFTLLPISAIYASYTLVFTVLRMSNEGRKALVT 240
QY 241 CSNHLIVGMFYGAATFMVLPSSFSHPKODNIISVFTYITVPALNPLIYSLRNKEVMA 300
DB 241 CSNHLIVGMFYGAATFMVLPSSFSHPKODNIISVFTYITVPALNPLIYSLRNKEVMA 300
QY 301 LRRVIGKYLILAH 313
DB 301 LRRVIGKYLILAH 313
DB 301 LRRVIGKYLILAH 313

RESULT 9
Q9VF88 PRELIMINARY; PRT; 315 AA.
AC Q9VF88;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Olfactory receptor MOR283-9 (Olfactory receptor
receptor GA_x6K0212PBj9-9067220-9068273).
GN GA_x6K0212PBj9-9067220-9068273.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]

```

RP SEQUENCE FROM N.A.
 RA Zhang X., Firestein S.J.;
 RT "The olfactory receptor gene superfamily of the mouse."
 RN Nat. Neurosci. 0:0-0(2002).
 [12]
 RP SEQUENCE FROM N.A.
 RA Adams M.;
 RN Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 [13]
 RP SEQUENCE FROM N.A.
 RA Young J.M., Shykind B.M., Lane R.P., Tomnes-Fridly L., Ross J.A.,
 Walker M., Williams E.M., Axel R., Trask B.J.;
 RT "Odorant receptor ESTs demonstrate olfactory expression of over 400
 genes, extensive alternate splicing, and unequal expression levels."
 RN Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 [14]
 RP SEQUENCE FROM N.A.
 RA Sanders K.;
 RN Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AY073646; AAL61309.1; -.
 DR EMBL: AY073646; AAL61309.1; -.
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0004872; F:receptor activity; IEA.
 DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSIN.
 DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KM Receptor
 SQ SEQUENCE 315 AA; 34927 MW; 9A9E426357BA710C CRC64;
 Query Match 77.6%; Score 1243; DB 11; Length 315;
 Best Local Similarity 78.8%; Pred. No. 9.9e-103;
 Matches 242; Conservative 29; Mismatches 36; Indels 0; Gaps 0;
 QY 1 MELNSTLGSGLVGLVGLDGSPELLVATFTLYMLATLTSNGLLLATITTEARLHMPY 60
 DB 1 MEVNSTLGSGLVGLVGLDGSPELLCAITLALYFALTSNGLLLVITWDARLHMPY 60
 QY 61 LLLGQLSLMDLLFTSVTPPKALADFLRENTISFGCALQMFELATMGSAEDLLAFMAY 120
 DB 61 LLLGQLSLMDLLFTSVTPPKALADFLRENTISFGCALQMFELATMGSAEDLLAFMAY 120
 QY 121 DRYVAICHPKLYMTSPRCVIMVATSWILASLAIAGHTWYTHLPFCVSWELRHLLCE 180
 DB 121 DRYVAICHPKLYMTSPRCVIMVATSWILASLAIAGHTWYTHLPFCVSWELRHLLCE 180
 QY 121 DRYVAICHPKLYMTSPRCVIMVATSWILASLAIAGHTWYTHLPFCVSWELRHLLCE 180
 DB 121 DRYVAICHPKLYMTSPRCVIMVATSWILASLAIAGHTWYTHLPFCVSWELRHLLCE 180
 QY 181 IPELKLKACDTSRELYIYVGVTELLPTSAIVASTYLVLFVLMPSNEGKKALVT 240
 DB 181 IPELKLKACDTSRELYIYVGVTELLPTSAIVASTYLVLFVLMPSNEGKKALVT 240
 QY 241 CSSHLIVGMYGAAATMYVLPSPFSPKODNIISVFYITVPALNPLIYSLRNKEVRA 300
 DB 241 CSSHLIVGMYGAAATMYVLPSPFSPKODNIISVFYITVPALNPLIYSLRNKEVRA 300
 QY 301 LRRVLGK 307
 DB 301 LRRVLGK 307
 RESULT 10
 Q7TRN4 PRELIMINARY; PRT; 311 AA.
 AC 07TRN4;
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Olfactory receptor GA_x6K0212PB09-9130754-9129519.
 GN GA_X6K0212PB09-9130754-9129519.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Young J.M., Shykind B.M., Lane R.P., Tomnes-Fridly L., Ross J.A.,
 Walker M., Williams E.M., Axel R., Trask B.J.;
 RT "Odorant receptor ESTs demonstrate olfactory expression of over 400
 genes, extensive alternate splicing, and unequal expression levels."
 RN Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 [12]
 RP SEQUENCE FROM N.A.
 RA Sanders K.;
 RN Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AY073646; AAL61309.1; -.
 DR EMBL: AY073646; AAL61309.1; -.
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0004872; F:receptor activity; IEA.
 DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 Query Match 77.2%; Score 1236; DB 11; Length 311;
 Best Local Similarity 77.9%; Pred. No. 4.1e-102;
 Matches 239; Conservative 31; Mismatches 37; Indels 0; Gaps 0;
 QY 1 MELNSTLGSGLVGLVGLDGSPELLVATFTLYMLATLTSNGLLLATITTEARLHMPY 60
 DB 1 MELNSTLGSGLVGLVGLDGSPELLCAITLALYFALTSNGLLLVITWDARLHMPY 60
 QY 61 LLLGQLSLMDLLFTSVTPPKALADFLRENTISFGCALQMFELATMGSAEDLLAFMAY 120
 DB 61 LLLGQLSLMDLLFTSVTPPKALADFLRENTISFGCALQMFELATMGSAEDLLAFMAY 120
 QY 121 DRYVAICHPKLYMTSPRCVIMVATSWILASLAIAGHTWYTHLPFCVSWELRHLLCE 180
 DB 121 DRYVAICHPKLYMTSPRCVIMVATSWILASLAIAGHTWYTHLPFCVSWELRHLLCE 180
 QY 121 DRYVAICHPKLYMTSPRCVIMVATSWILASLAIAGHTWYTHLPFCVSWELRHLLCE 180
 DB 121 DRYVAICHPKLYMTSPRCVIMVATSWILASLAIAGHTWYTHLPFCVSWELRHLLCE 180
 QY 181 IPELKLKACDTSRELYIYVGVTELLPTSAIVASTYLVLFVLMPSNEGKKALVT 240
 DB 181 IPELKLKACDTSRELYIYVGVTELLPTSAIVASTYLVLFVLMPSNEGKKALVT 240
 QY 241 CSSHLIVGMYGAAATMYVLPSPFSPKODNIISVFYITVPALNPLIYSLRNKEVRA 300
 DB 241 CSSHLIVGMYGAAATMYVLPSPFSPKODNIISVFYITVPALNPLIYSLRNKEVRA 300
 QY 301 LRRVLGK 307
 DB 301 LRRVLGK 307
 RESULT 11
 Q8VFM6 PRELIMINARY; PRT; 311 AA.
 AC 08VFM6;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Olfactory receptor MOR283-3.
 GN Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang X., Firestein S.J.;
 RT "The olfactory receptor gene superfamily of the mouse."
 RN Nat. Neurosci. 0:0-0(2002).
 [12]
 RP SEQUENCE FROM N.A.
 RA Adams M.;
 RN Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AY073495; AAL61158.1; -.
 DR EMBL: AY073495; AAL61158.1; -.
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0004872; F:receptor activity; IEA.
 DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS50262; G_PROTEIN_RECIP_FL_2; 1.
KW RECEPTOR

SEQUENCE 311 AA; 34194 MW; 90113F7C8BF8D20C CRC64;
Query Match 76.8%; Score 1230; DB 11; Length 311;
Best Local Similarity 77.5%; Pred. No. 1.4e-101;
Matches 238; Conservative 31; Mismatches 38; Indels 0; Gaps 0;

QY 1 MELNSTLGSGLFVILVGLNDGSPDLLYATFTIYMLALNSGILLALITTEARLHMPY 60
DB 1 MELNSTLGSGLFVILVGLNDGSPDLLYATFTIYMLALNSGILLALITTEARLHMPY 60
QY 61 LLLGQSLMDLFLSVTPKALDPLRENTISFGGCAQMFALTMGSAEDLLAFMAY 120
DB 61 LLLGQSLMDLFLSVTPKALDPLRENTISFGGCAQMFALTMGSAEDLLAFMAY 120
QY 121 DRYVAICHPKMYTMSPRVCMVATSWILASIALGHTMYTMHLPCVSWETRIHCE 180
DB 121 DRYVAICHPKMYTMSPRVCMVATSWILASIALGHTMYTMHLPCVSWETRIHCE 180
QY 181 IPELKLKACADTSRYELIIVTGVTFLLPISAVASYTLVFTVLMPSNEGRKKALVT 240
DB 181 IPELKLKACADTSRYELIIVTGVTFLLPISAVASYTLVFTVLMPSNEGRKKALVT 240
QY 241 CSSHLIVGMFYGAATMYTLPSFSFHPKQDNISVYTTVTPALNPLIYSLNKEYWRA 300
DB 241 CSSHLIVGMFYGAATMYTLPSFSFHPKQDNISVYTTVTPALNPLIYSLNKEYWRA 300
QY 301 LRRVLTGR 307
DB 301 LRRVLTGR 307

RESULT 12

Q8VFM3
ID 08VFM3 PRELIMINARY; PRT; 315 AA.

AC 08VFM3;
DT 01-MAR-2002 (TEMBLrel. 20, Created)
DT 01-MAR-2003 (TEMBLrel. 20, Last sequence update)
DE 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Olfactory receptor MOR283-6 (Olfactory receptor
GA_X6K02T2PBJ9-9092181-9091234).
GN GA_X6K02T2PBJ9-9092181-9091234.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang X., Firestein S.J.;
RT "The olfactory receptor gene superfamily of the mouse.";
RL Nat. Neurosci. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Adams M.;
RN Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Young J.M., Shykind B.M., Lane R.P., Tomnes-Priddy L., Rose J.A.,
RA Walker M., Williams B.M., Axel R., Trask B.J.;
RT "Odorant receptor ESTs demonstrate olfactory expression of over 400
genes, extensive alternate splicing, and unequal expression levels.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Sanders K.;
RN Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY073499; AAL61162.1; -
DR EMBL; AY317816; AAP71161.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS50262; G_PROTEIN_RECIP_FL_2; 1.
KW RECEPTOR

SEQUENCE 315 AA; 35179 MW; AC02001D73D1736 CRC64;
Query Match 75.6%; Score 1210.5; DB 11; Length 315;
Best Local Similarity 75.2%; Pred. No. 7.8e-100;
Matches 237; Conservative 31; Mismatches 46; Indels 1; Gaps 1;

QY 1 MELNSTLGSGLFVILVGLNDGSPDLLYATFTIYMLALNSGILLALITTEARLHMPY 60
DB 1 MELNSTLGSGLFVILVGLNDGSPDLLYATFTIYMLALNSGILLALITTEARLHMPY 60
QY 61 LLLGQSLMDLFLSVTPKALDPLRENTISFGGCAQMFALTMGSAEDLLAFMAY 120
DB 61 LLLGQSLMDLFLSVTPKALDPLRENTISFGGCAQMFALTMGSAEDLLAFMAY 120
QY 121 DRYVAICHPKMYTMSPRVCMVATSWILASIALGHTMYTMHLPCVSWETRIHCE 180
DB 121 DRYVAICHPKMYTMSPRVCMVATSWILASIALGHTMYTMHLPCVSWETRIHCE 180
QY 181 IPELKLKACADTSRYELIIVTGVTFLLPISAVASYTLVFTVLMPSNEGRKKALVT 240
DB 181 IPELKLKACADTSRYELIIVTGVTFLLPISAVASYTLVFTVLMPSNEGRKKALVT 240
QY 241 CSSHLIVGMFYGAATMYTLPSFSFHPKQDNISVYTTVTPALNPLIYSLNKEYWRA 300
DB 241 CSSHLIVGMFYGAATMYTLPSFSFHPKQDNISVYTTVTPALNPLIYSLNKEYWRA 300
QY 301 LRRVLTGR 315
DB 301 LRRVLTGR 315

RESULT 13

Q8VFM3
ID 08VFM3 PRELIMINARY; PRT; 316 AA.

AC 08VFM3;
DT 01-MAR-2002 (TEMBLrel. 20, Created)
DT 01-MAR-2003 (TEMBLrel. 20, Last sequence update)
DE 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Olfactory receptor MOR283-8 (Olfactory receptor
GA_X6K02T2PBJ9-9055944-9054994).
GN GA_X6K02T2PBJ9-9055944-9054994.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang X., Firestein S.J.;
RT "The olfactory receptor gene superfamily of the mouse.";
RL Nat. Neurosci. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Adams M.;
RN Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Young J.M., Shykind B.M., Lane R.P., Tomnes-Priddy L., Rose J.A.,
RA Walker M., Williams B.M., Axel R., Trask B.J.;
RT "Odorant receptor ESTs demonstrate olfactory expression of over 400
genes, extensive alternate splicing, and unequal expression levels.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Sanders K.;
RN Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY073499; AAL61308.1; -
DR EMBL; AY317814; AAP71159.1; -

DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0004872; P: receptor activity; IEA.
 DR GO: GO:0001584; P: rhodopsin-like receptor activity; IEA.
 DR GO: GO:0007186; P: G-protein coupled receptor protein signalin. . . ; IEA.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm 1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS50262; G_PROTEIN_RECER_F1_2; 1.
 KM RECEPTOR
 SQ SEQUENCE 316 AA; 35153 MW; 2123AF7831AFA228 CRC64;
 Query Match 75.2%; Score 1205; DB 11; Length 316;
 Best Local Similarity 73.8%; Pred. No. 2.4e-99;
 Matches 231; Conservative 36; Mismatches 46; Indels 0; Gaps 0;
 QY 1 MELNSTLGSGLVIGLINDSGSPFLYATFTIYMLALTSNGILLATITLRLHMPY 60
 DB 1 MEPNSTLGSGLVIGLINDSGSPFLCATITLALYMLALISGMILITMDIYLVPMY 60
 QY 61 LLLGSLMDLFTSVTPKALADFLRENTISFGCALQMFALITMGSAEDLLAFMAY 120
 DB 61 LLLGSLMDLFTSVTPKALADFLRENTISFGCALQMFALITMGSAEDLLAFMAY 120
 QY 121 DRYVAICHLKMYTMSPRVCIMVATSWILASLAIQHTMYMLPCVSWETRHLC 180
 DB 121 DRYVAICHLKMYTMSPRVCIMVATSWILASLAIQHTMYMLPCVSWETRHLC 180
 QY 181 IPELLKACADTSRELIITYGTFTLLPSAIYASTVLFTYLRMPSNEGRKALVT 240
 DB 181 IPELLKACADTSRELIITYGTFTLLPSAIYASTVLFTYLRMPSNEGRKALVT 240
 QY 241 CSSHLIVGMFYGATFMYVLPSSFSHPKODNIISVFITVTPALNPYISLRNKEV 300
 DB 241 CSSHLIVGMFYGATFMYVLPSSFSHPKODNIISVFITVTPALNPYISLRNKEV 300
 QY 301 LRRVLGKYLLAH 313
 DB 301 LRRVLGKYLLAH 313
 QY 301 LRRVLGKYLLAH 313
 DB 301 LRRVLGKYLLAH 313
 RESULT 14
 Q8VFEM4 PRELIMINARY; PRT; 317 AA.
 AC Q8VFEM4
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Olfactory receptor MOR283-5 (Olfactory receptor
 DE GA_X6K02T2PB3J-9119301-9118348).
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RA SEQUENCE FROM N.A.
 RT "The olfactory receptor gene superfamily of the mouse."
 RL Nat. Neurosci. 0:0-0(2002).
 RN [2]
 RA SEQUENCE FROM N.A.
 RT Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RA SEQUENCE FROM N.A.
 RT Young J.M., Shykind B.M., Lane R.P., Tonnes-Priiddy L., Ross J.A.,
 RA Walker M., Williams B.M., Axel R., Trask B.D.;
 RT "Odorant receptor ESTs demonstrate olfactory expression of over 400
 RT genes, extensive alternate splicing, and unequal expression levels."
 RT Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RA SEQUENCE FROM N.A.
 RT Sanders K.;

RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY073498; AAL61161.1; -
 DR EMBL: AY317818; AAP71162.1; -
 DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0004872; P: receptor activity; IEA.
 DR GO: GO:0001584; P: rhodopsin-like receptor activity; IEA.
 DR GO: GO:0007186; P: G-protein coupled receptor protein signalin. . . ; IEA.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm 1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS50262; G_PROTEIN_RECER_F1_2; 1.
 KM RECEPTOR
 SQ SEQUENCE 317 AA; 35471 MW; C5F1B706E5437F73 CRC64;
 Query Match 75.2%; Score 1204; DB 11; Length 317;
 Best Local Similarity 75.5%; Pred. No. 3e-99;
 Matches 231; Conservative 29; Mismatches 46; Indels 0; Gaps 0;
 QY 1 MELNSTLGSGLVIGLINDSGSPFLYATFTIYMLALTSNGILLATITLRLHMPY 60
 DB 1 MEPNSTLGSGLVIGLINDSGSPFLCATITLALYMLALISGMILITMDIYLVPMY 60
 QY 61 LLLGSLMDLFTSVTPKALADFLRENTISFGCALQMFALITMGSAEDLLAFMAY 120
 DB 61 LLLGSLMDLFTSVTPKALADFLRENTISFGCALQMFALITMGSAEDLLAFMAY 120
 QY 121 DRYVAICHLKMYTMSPRVCIMVATSWILASLAIQHTMYMLPCVSWETRHLC 180
 DB 121 DRYVAICHLKMYTMSPRVCIMVATSWILASLAIQHTMYMLPCVSWETRHLC 180
 QY 181 IPELLKACADTSRELIITYGTFTLLPSAIYASTVLFTYLRMPSNEGRKALVT 240
 DB 181 IPELLKACADTSRELIITYGTFTLLPSAIYASTVLFTYLRMPSNEGRKALVT 240
 QY 241 CSSHLIVGMFYGATFMYVLPSSFSHPKODNIISVFITVTPALNPYISLRNKEV 300
 DB 241 CSSHLIVGMFYGATFMYVLPSSFSHPKODNIISVFITVTPALNPYISLRNKEV 300
 QY 301 LRRVLG 306
 DB 301 LRRVLG 306
 QY 301 LRRVLG 306
 DB 301 LRRVLG 306
 RESULT 15
 Q9EPF6 PRELIMINARY; PRT; 315 AA.
 AC Q9EPF6
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE T3 olfactory receptor (Olfactory receptor
 DE GA_X6K02T2PB3J-9247095-9248042).
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RA SEQUENCE FROM N.A.
 RT STRAIN=C57BL/6J;
 RC MEDLINE=21310002; PubMed=11416212;
 RX Lane R.P., Cutforth T., Young J., Athanasiou M., Friedman C.,
 RA Rowen L., Evans G., Axel R., Hood L., Trask B.D.;
 RT "Genomic analysis of orthologous mouse and human olfactory receptor
 RT loci."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:7390-7395(2001).
 RN [2]
 RA SEQUENCE FROM N.A.
 RT Young J.M., Shykind B.M., Lane R.P., Tonnes-Priiddy L., Ross J.A.,
 RA Walker M., Williams B.M., Axel R., Trask B.D.;
 RT "Odorant receptor ESTs demonstrate olfactory expression of over 400
 RT genes, extensive alternate splicing, and unequal expression levels."
 RT Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RL

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RN [3]
RP SEQUENCE FROM N.A.
RA Sanders K.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF321234; AAG45197.1; -.
DR EMBL; AY317825; AAP7169.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; P:G-protein-coupled receptor protein signaling; IEA.
DR GO; GO:0007186; P:G-protein-coupled receptor protein signaling; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS50262; G_PROTEIN_REC_F1_2; 1.
KM Receptor.
SQ SEQUENCE 315 AA; 35119 MW; 4ECD3A2FE3B41030 CRC64;

Query Match 75.1%; Score 1203; DB 11; Length 315;
Best Local Similarity 76.2%; Pred. No. 3,6e-99;
Matches 234; Conservative 33; Mismatches 40; Indels 0; Gaps 0;

QY 1 MELRNSTLGGFTLVGILNDGSPDLIYATFTIYMLATNSGLLAIITEARLAMPY 60
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   1 MEVNSTLRSGFTIMGILDNDPELLCATTALYLAITSNGHLLVITMDTRLHVMY 60

DB 61 LLLGQSLMDLFTSVTPKALADELRRENTISFGCALOMFLATMGSAEDLLAFMY 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   61 LLMQLSLMDLFTSVTPKALADYLDLNDNTISFGCALOMFLATMGTAEDLLAFMY 120

QY 121 DRYVAICHPLKMYMTLMSPRVCMVATSWILASLAIAGHTMYTWHLPECVSWEIRHLCE 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   121 DRYVAICHPLNTYITLMSQKCCIMATSMIASLSALGYSMYTMQYFCKSRQIRHLCE 180

DB 181 IPPLLKLIACADTSRYEELIIVTGVTFLLPISAVASYTLVFTVLMPSNENGRKALVT 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   181 IPPLLKLIACADTSRYEELIIVTGVTFLLPISAVASYTLVFTVLMPSNENGRKALVT 240

QY 241 CSSHLIVGMVFGAATMYVLPSFHSFKODNITSVYITVTPALNPLIYSLRNKEYMRA 300
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   241 CSSHLIVGMVFGAATMYVLPSFHSFKODNITSVYITVTPALNPLIYSLRNKEYMRA 300

DB 301 LRRVLGK 307
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   301 LRRVLGK 307
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Search completed: August 18, 2004, 08:58:37
Job time : 80 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2004, 08:55:13 ; Search time 19 Seconds

(without alignments)
858,621 Million cell updates/sec

Title: US-10-024-444B-2

Sequence: 1602
1 MELRNSTLGSGLVIGLIND.....VMRLRVKYLIAHSTL 316

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	792	49.4	316	2	US-08-827-291A-2
2	668	41.7	321	3	US-08-748-506-12
3	666	41.6	321	3	US-08-748-506-20
4	663.5	41.4	321	3	US-08-748-506-10
5	661.5	41.3	321	3	US-08-748-506-13
6	661.5	41.3	321	3	US-08-748-506-18
7	644	40.2	340	4	US-09-546-986A-6
8	644	40.2	340	4	US-09-524-730-6
9	643	40.1	321	3	US-08-748-506-19
10	642	40.1	223	4	US-09-465-901-40
11	642	40.1	321	3	US-08-748-506-11
12	632	39.5	314	3	US-08-988-876-7
13	616	38.5	334	4	US-09-546-986A-8
14	616	38.5	334	4	US-09-524-730-8
15	605	37.8	310	4	US-09-546-986A-2
16	605	37.8	310	4	US-09-524-730-2
17	595.5	37.2	313	4	US-09-465-901-48
18	582	36.3	284	5	US-08-118-270-61
19	582	36.3	284	5	PCT-US93-08528-61
20	577.5	36.0	296	2	US-08-467-947A-2
21	577.5	36.0	296	2	US-08-467-947A-2
22	576	36.0	333	3	US-08-988-876-6
23	575	35.9	309	3	US-08-988-876-5
24	575	35.9	331	4	US-09-546-986A-4
25	565.5	35.3	284	1	US-09-524-730-4
26	565.5	35.3	284	1	US-08-118-270-67
27	565.5	35.3	284	5	PCT-US93-08528-67

28	563	35.1	223	4	US-09-465-901-24	Sequence 24, Appl
29	558	34.8	223	4	US-09-465-901-20	Sequence 20, Appl
30	558	34.8	223	4	US-09-465-901-28	Sequence 28, Appl
31	534.5	33.4	274	1	US-08-118-270-69	Sequence 69, Appl
32	534.5	33.4	274	1	PCT-US93-08528-69	Sequence 69, Appl
33	516	32.2	277	1	US-08-118-270-68	Sequence 68, Appl
34	516	32.2	277	1	PCT-US93-08528-68	Sequence 68, Appl
35	512.5	32.0	286	1	US-08-118-270-65	Sequence 65, Appl
36	512.5	32.0	286	1	PCT-US93-08528-65	Sequence 65, Appl
37	507	31.6	247	1	US-08-465-980-3	Sequence 3, Appl1
38	507	31.6	247	2	US-09-053-303-3	Sequence 3, Appl1
39	507	31.6	247	4	US-09-339-115-3	Sequence 3, Appl1
40	507	31.6	247	5	PCT-US93-07093-3	Sequence 3, Appl1
41	500	31.2	223	4	US-09-465-901-38	Sequence 38, Appl
42	496.5	31.0	222	2	US-08-467-948A-27	Sequence 27, Appl
43	496.5	31.0	222	3	US-08-467-947A-27	Sequence 27, Appl
44	495.5	30.9	293	1	US-08-118-270-60	Sequence 60, Appl
45	495.5	30.9	293	5	PCT-US93-08528-60	Sequence 60, Appl

ALIGNMENTS

RESULT 1
US-08-827-291A-2
; Sequence 2, Application US/08827291A
; Patent No. 5874243

GENERAL INFORMATION:

APPLICANT: Macina, Roberto
TITLE OF INVENTION: NOVEL OLRC15 RECEPTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA

COUNTRY: PA

ZIP: 19406

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/827,291A

FILING DATE: 28-MAR-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: King, William T

REGISTRATION NUMBER: 30,954

REFERENCE/DOCKET NUMBER: GP50001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-270-5015

TELEFAX: 610-270-5090

TELEX:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 316 amino acids

TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-827-291A-2

Query Match 49.4%; Score 792; DB 2; Length 316;
Best Local Similarity 49.5%; Pred. No. 7,86-65;
Matches 152; Conservative 49; Mismatches 106; Indels 0; Gaps 0;

Db 1 MARENSTNSDFIFLGIENHSPHTLFLVLAIFVAFMGNSVWLLIYDTQHTPMX 60
 QY 61 LILGQISLMDLFTSVVTPKALADFLRRENTISFGGALQMFALTMGSAEDLLAFMA 120
 Db 61 LILGQISLMDLFTSVVTPKALADFLRRENTISFGGALQMFALTMGSAEDLLAFMA 120
 QY 121 DRVVAICHPKXWTLMSPRCWMVATSMVSLAIIAGHTMYMHLPCVSWERHLLCE 180
 Db 121 DRVVAICHPKXWTLMSPRCWMVATSMVSLAIIAGHTMYMHLPCVSWERHLLCE 180
 QY 181 IPELKLACADTSRYELIIVVTGTFLLPISAIVASVTLVLTFLRMPSEGRKALVT 240
 Db 181 IPELKLACADTSRYELIIVVTGTFLLPISAIVASVTLVLTFLRMPSEGRKALVT 240
 QY 241 CSSHLIVMGFGAALFMYLPSFSHPKODNISVFTYVTPALPLIYSLNKXVMA 300
 Db 241 CSSHLIVMGFGAALFMYLPSFSHPKODNISVFTYVTPALPLIYSLNKXVMA 300
 QY 301 LRRVLGK 307
 Db 301 LRRVLGK 307
 QY 301 FMKISGK 307
 Db 301 FMKISGK 307

RESULT 2
 US-08-748-506-12
 / Sequence 12, Application US/08748506
 / Patent No. 6159707

GENERAL INFORMATION:
 APPLICANT: Ronnett et al.
 TITLE OF INVENTION: NOVEL SPERM RECEPTORS
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Leydig, Volt & Mayer, Ltd.
 STREET: Two Prudential Plaza, Suite 4900
 CITY: Chicago
 STATE: IL
 COUNTRY: US
 ZIP: 60601-6780
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/748,506
 FILING DATE: 08-NOV-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/033,751
 FILING DATE: 09-NOV-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 REFERENCE/DOCKET NUMBER: 74940
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-616-5600
 TELEFAX: 312-616-5700
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 321 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-748-506-12

Query Match 41.7%; Score 668; DB 3; Length 321;
 Best Local Similarity 47.3%; Pred. No. 1.8e-53;
 Matches 133; Conservative 42; Mismatches 106; Indels 0; Gaps 0;

QY 26 LLYATFTILYMLATNSGLLATTIERARLHMPYLLIGQISLMDLFTSVVTPKALAD 85
 Db 32 LLYATFTILYMLATNSGLLATTIERARLHMPYLLIGQISLMDLFTSVVTPKALAD 85

QY 86 LRRENTISFGGALQMFALTMGSAEDLLAFMAVDRVVAICHPKXWTLMSPRCWMV 145
 Db 92 VSEARGISWEGCASQMFPIFGITECCLLAAMAFDRVVAICSPHVAATRMGRGCAVLA 151
 QY 146 ATSMVSLAIIAGHTMYMHLPCVSWERHLLCEIPPLKLACADTSRYELIIVTGV 205
 Db 152 IVSWWGICVIGQINFISLNEGCEIDHFCEDLPPLALACGDISQNEAIFPAVNL 211
 QY 206 FLLPISAIVASVTLVLTFLRMPSEGRKALVTSSHLIVMGFGAALFMYLPSFS 265
 Db 212 CIFSPFLLISSVRLVAVLWMPSEGRHKALSTSSHLVTLVTFGTSATYLRSSKS 271
 QY 266 HSPKODNISVFTYVTPALPLIYSLNKXVMAVLRVIG 306
 Db 272 HSPGVDKLALFYTSTVSMPLIYSLNKXVMAVLRVIG 312

RESULT 3
 US-08-748-506-20
 / Sequence 20, Application US/08748506
 / Patent No. 6159707

GENERAL INFORMATION:
 APPLICANT: Ronnett et al.
 TITLE OF INVENTION: NOVEL SPERM RECEPTORS
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Leydig, Volt & Mayer, Ltd.
 STREET: Two Prudential Plaza, Suite 4900
 CITY: Chicago
 STATE: IL
 COUNTRY: US
 ZIP: 60601-6780
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/748,506
 FILING DATE: 08-NOV-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/033,751
 FILING DATE: 09-NOV-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 REFERENCE/DOCKET NUMBER: 74940
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-616-5600
 TELEFAX: 312-616-5700
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 321 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-748-506-20

Query Match 41.6%; Score 666; DB 3; Length 321;
 Best Local Similarity 47.3%; Pred. No. 2.7e-53;
 Matches 133; Conservative 42; Mismatches 106; Indels 0; Gaps 0;

QY 26 LLYATFTILYMLATNSGLLATTIERARLHMPYLLIGQISLMDLFTSVVTPKALAD 85
 Db 32 LLYATFTILYMLATNSGLLATTIERARLHMPYLLIGQISLMDLFTSVVTPKALAD 85

QY 86 LRRENTISFGGALQMFALTMGSAEDLLAFMAVDRVVAICHPKXWTLMSPRCWMV 145
 Db 92 VSEARGISWEGCASQMFPIFGITECCLLAAMAFDRVVAICSPHVAATRMGRGCAVLA 151

QY 146 ATSMVSLAIIAGHTMYMHLPCVSWERHLLCEIPPLKLACADTSRYELIIVTGV 205
 Db 152 IVSWWGICVIGQINFISLNEGCEIDHFCEDLPPLALACGDISQNEAIFPAVNL 211

QY 20 FLILPILAIYAATLVLFVFLRMPSEEGKKLLVTCSSHLIVMGFGAALFEMVLSSP 266
 Db 212 CIFSPFLILISVRLIVLVMPSEEGKKLLSTCSSHLIVTLFVFSYATYLRKSS 271
 QY 266 HSPQDNILISVFTYLPALNPILYSLRKVEYKALRRVLG 306
 Db 272 HSPQDNLALFYTIVSKMLNPILYSLRKVEYKALRRVLTG 312

RESULT 4

```

US-08-748-506-10
Sequence 10, Application US/08748506
Patent No. 6159707
GENERAL INFORMATION:
APPLICANT: Romnec et al.
TITLE OF INVENTION: NOVEL SPERM RECEPTORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Volt & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: US
ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,506
FILING DATE: 08-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,751
FILING DATE: 09-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 74940
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5600
TELEFAX: 312-616-5700
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-748-506-10

```

Query Match	41.4%;	Score 663.5;	DB 3;	Length 321;
Best Local Similarity	-47.9%;	Pred. No. 4.6e-53;		
Matches 137, Conservative	39;	Mismatches 109;	Indels 1;	Gaps 1

QY 26 LIIAFTLLIYMLALTSNGLLIALLATTEARLHMEPYLLIGOLSLMDLLEFSVTPEKALADF 85
 Db 32 LIFNNLLIFSVLSIGNLLIVAIATCSPTSLTTPYFFELANLSLEIGYTCSPVPEKLGSL 91
 QY 86 IARENTTISFGGCAIMFALTMGSAEDLLAFMYADYVAICHPDIKMTLSRVCIMIV 145
 Db 92 VSEAREISREGATQMFPPAFPGITTECLLAAMAFDCMAICSPRLHYATMTSEVCAHIA 151
 QY 146 ANSYLLASHLAIAGHTMTYMLPFCVSWERHLLCEIPRLKLAACADTSREYELLIVYTGVT 205
 Db 152 IYVSWGCVISLGGTNPIFSLNFPGCEIDHFFCDLPELLALACGTSQNEAIRFVAVL 211
 QY 206 FLLELISAIIVASYTLVLEFTVLKMPNSNEERKALATGCSHLIYVAMPFGAATFMYVLPSSE 265
 Db 212 CTSPPFLIIIVSYVKILAVLAMPSPERKHALLTSCSHLIVTLRFGASCTIYLPKXS 271
 QY 266 HSPKODNIIISVYTTIVTPALNPLIYLSRNKEVMAALRRVIG-KYIL 310

Db 272 HSPGMDKELAFYTVTSMINPIIYSLRNKEVKAAALRRTLGKKIL 317

RESULT 5

```

US-08-748-506-13
Sequence 13, Application US/08748506
Patent No. 6159707
GENERAL INFORMATION:
APPLICANT: Rognett et al.
TITLE OF INVENTION: NOVEL SPERM RECEPTORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Volt & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: US
ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,506
FILING DATE: 08-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,751
FILING DATE: 09-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 74940
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5600
TELEFAX: 312-616-5700
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-748-506-13

```

Query Match	41.3%;	Score 661.5;	DB 3;	Length 321;
Best Local Similarity	46.9%;	Pred. No. 7e-53;		
Matches 134;	Conservative 42;	Mismatches 109;	Indels 1;	Gaps 1

Qy	2 L I V A F E T T I U M A L S N C E L L A T I T B A R L H M P Y L L G O L S I M D L F S V P K X A L A P	85
Dd	32 L I F T L I L M E F V S L T G N M L I A I C T S P S L T E M Y F F L A N S L E I G T O S V I P K M Q S I	91
Qy	86 L R R E N T I S E G C A L O M E L T A L T M G S A E D L L A F M A Y D R Y V A I C H P E K M T L M S D R V C W I M V	145
Dd	92 V E A E R E I F O V G A T O M F F E I F F G I T E C C L A A M A F D R Y M A I C S P L H A T R M S R E V C A H A	151
Qy	146 A V S W I L A S I A I G H M Y T M H . P C V S W E I H L C E I P P L K A C A D T S R E L I I Y V T G T	205
Dd	152 I Y S W M G C I V G L G C T N F I F S L N F C G P C E I D H F C D P L P A L A C G D T S Q I E A N I F V V V A	211
Qy	206 F L L D I P I S A I V A S Y T L V L F T Y L R M S N E G R K K A V T C S H L I V Y G M E Y G A T F M V I P S S F	265
Dd	212 C I S S E F L I I S Y A I V A V A V M P S P E G R K H A L S T C S H L I V T L F F G S G S V T Y L P K S S	271
Qy	266 H S P K O D N I S V P T I Y P A L N E L Y S I R E N E W R A I R V U G - K Y I L	310
Dd	272 H S P G M D K I A L P Y A V T S M L N P I I Y S I R A N D O V G A L R R I I A L K K I L	317

RESULT 6

US-08-748-506-18

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Sequence 18: Application US/08748506
Patent No. 6159707
GENERAL INFORMATION:
APPLICANT: Ronnett et al.
TITLE OF INVENTION: NOVEL SPERM RECEPTORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Volt & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: US
ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,506
FILING DATE: 08-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,751
FILING DATE: 09-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 74940
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5600
TELEFAX: 312-616-5700
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-748-506-18

Query Match 41.3%; Score 661.5; DB 3; Length 321;
Best Local Similarity 47.9%; Pred. No. 7e-53;
Matches 137; Conservative 39; Mismatches 109; Indels 1; Gaps 1

QY 26 LLYATFTTIVMLALTSNGLLIATITTEARLHMPMYLLIGOLSLMDLFTSVTPRALAD 85
DB 32 LLLPMLILMFLVSLGNTLLIYALITSTPSLHPTMVFLLANLSLIRIGTCSVIPMLQSL 91
QY 86 LRENTTISFGGCAOMFLATLMGSAEDLLAFMAYDRYVALCHPLKXWTLSPRKWTMLN 145
DB 92 VSEAREISREGCATOMFEFFAFGITECCILAMAFDRCAICSPLAHYATMSREVCALHA 151
QY 146 ATSMILASLLIAGHMYTMHLDFGCSWEIRHLCEIPPLTLKACADTSRYELIIVTGV 205
DB 152 IVSWMGCVISIGQTNFIPLSNFCGPCIIDHFCDLPELLALACDPTQNEALITVAVL 211
QY 206 FLPLPISATVASYTLVLFPTVLMPSENGRKKALVTCSSHLIVGMFYGAATFMYVLPSS 265
DB 212 CTSPPFLILIVSYVILLIIVLLMPSEGRKHALTSCSSHLIVTTLFYGACACTYLRPKSS 271
QY 266 HSPKODNIIISVFTYVTPALNPLIISLNKEVMALRPVLG-KYLL 310
DB 272 HSPGDKFLALFYIVVTSMLNPLIISLNKEVAAALRRTLGAKLL 317

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[illegible]

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Db      79 PMVFPLANISFLMSFTTISVLPOLLANLWGPQKTIISVGGCWQPFYISHMLGAIECVILAT 138
QY      118 MAYDRVAIAICHPKXTMTLSPRVCMVATSWTILASLIAIGHMTYTMHLPCVSWETRHL 177
Db      139 MSYDRVAIAICHPKXTMTLSPRVCMVATSWTILASLIAIGHMTYTMHLPCVSWETRHL 198
QY      178 LGEIPLKACADTSRYELIIVTGVTLPLPISAVSYTLVFTVLRMPSENGRKA 237
Db      199 FCEMPLIMQACVDTISLNMENMLASVFEVPLGLILVSYGHIAVAKIRSAEGRRA 258
QY      238 LVTCSHLLIVGMFGAATPMVLPSSFSHPKODNIISVEYITVTPALNPLISLRNKEY 297
Db      259 FMTCSGHVAVSLFVYSIIFMVLQPAKSHSEGRKIALFYVTVTALNPLIITLNTXY 318
QY      298 MPALRRVL 305
Db      319 KSALRRMV 326

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RESULT 9

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US-08-748-506-19
; Sequence 19, Application US/08748506
; Patent No. 6159707
; GENERAL INFORMATION:
; APPLICANT: Ronnett et al.
; TITLE OF INVENTION: NOVEL SPERM RECEPTORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voigt & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: US
; ZIP: 60601-6780
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,506
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,751
; FILING DATE: 09-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; REFERENCE/DOCKET NUMBER: 74940
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5600
; TELEFAX: 312-616-5600
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-748-506-19

```

```

Query Match      40.1%; Score 643; DB 3; Length 321;
Best Local Similarity 46.4%; Pred. No. 3.5e-51;
Matches 130; Conservative 39; Mismatches 111; Indels 0; Gaps 0;
QY      26 LLYATFTLIMLALNSGLILATITELARLHPVTLILGOLSTIMDLFTSVTPKALDF 85
Db      32 LILFTLILMLFVLSLGNALIALACTSPSLHPMTFLANISLLEIGTCSYIPMLQSL 91
QY      86 LRENTISFGGCAOMFLATLNGSAEDLLAFMAYDRVAIAICHPKXTMTLSPRVCMV 145
Db      92 VSEANEISREGCATOMFFFTFGITECCILAMAFDRCGICSPHAYATRMSREVCALHA 151

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QY      146 ATSMILASLIAIGHTMYTMHLPCVSWETRHLCEIPLPKACADTSRYELIIVTGV 205
Db      152 IYSWGGCIVGIGQTNINISLNFCECEIDHFECDPLPLALACGPTSQNEAIFVAAIL 211
QY      206 FLLPLISAIVASYTLVFTVLRMPSENGRKKALVTCSSHLIVGMFGAATPMVLPSSF 265
Db      212 CISPFLVILYSIVRLVAVLWPSPEGRKALSTSSHLVLTLPFGSVSFTYLRPKSS 271
QY      266 HSPKODNIISVEYITVTPALNPLIYSLRNKEYVRLARVL 305
Db      272 HSPGMDKLALFYTANTSMNLPIIYSLRNKEYVRLARVL 311

```

RESULT 10

```

US-09-465-901-40
; Sequence 40, Application US/09465901
; Patent No. 6492143
; GENERAL INFORMATION:
; APPLICANT: Reed, Randall
; APPLICANT: Yau, King-Wai
; APPLICANT: Krautwurst, Dietmar
; TITLE OF INVENTION: Olfactory Receptor Expression Libraries
; TITLE OF INVENTION: ad Methods of Making and Using Them
; FILE REFERENCE: 001107, 00105
; CURRENT APPLICATION NUMBER: US/09/465,901
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/112,605
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 223
; TYPE: PR
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-465-901-40

```

```

Query Match      40.1%; Score 642; DB 4; Length 223;
Best Local Similarity 55.7%; Pred. No. 2.8e-51;
Matches 123; Conservative 29; Mismatches 69; Indels 0; Gaps 0;
QY      66 ISMLPLFTSVTPKALDFLRENTISFGGCAOMFLATLNGSAEDLLAFMAYDRVA 125
Db      3 LSFIDMMYISTIVPMLVDYLLGQRTISFVGCTAQHFLYTLVGAEPFLGLMAYDRVA 62
QY      126 ICHPKXTMTLSPRVCMVATSWTILASLIAIGHTMYTMHLPCVSWETRHLCEIPL 185
Db      63 ICNPLKXTMTLSPRVCMVATSWTILASLIAIGHTMYTMHLPCVSWETRHLCEIPL 122
QY      186 KACADTSRYELIIVTGVTLPLPISAVSYTLVFTVLRMPSENGRKKALVTCSSHL 245
Db      123 KACADTSRYELIIVTGVTLPLPISAVSYTLVFTVLRMPSENGRKKALVTCSSHL 182
QY      246 IYGMFGAATPMVLPSSFSHPKODNIISVEYITVTPALN 286
Db      183 IVTLFYGAATYVWPVPSHSPSQDKIFSVYITLTPMLN 223

```

RESULT 11

```

US-08-748-506-11
; Sequence 11, Application US/08748506
; Patent No. 6159707
; GENERAL INFORMATION:
; APPLICANT: Ronnett et al.
; TITLE OF INVENTION: NOVEL SPERM RECEPTORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voigt & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: US

```

ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentia Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/748,506
FILING DATE: 08-NOV-1996
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/033,751
FILING DATE: 09-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION: 74940
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5600
TELEFAX: 312-616-5700
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-748-506-11

Query Match 40.1%; Score 642; DB 3; Length 321;
Best Local Similarity 46.4%; Pred. No. 4.3e-51;
Matches 130; Conservative 38; Mismatches 112; Indels 0; Gaps 0;

QY 26 LLYATFTILYMLALTSNGILLATITFARLHMPYLLIGLSIMDLFTSVVPMKALAD 85
DB 32 LFTLLMLVSLTGALLALXCTSPSLHTPYFPLANLSLEIGYTSVIPKMLQSL 91
QY 86 LRRENTISFGGALOMFLATMGSABDLLEAFAYDRYVAICHLKMYLMSPRVCWIV 145
DB 92 VSRARETSRGCAQTFQFFFTGTBCCLLAAMAFDCMGICSPHATMSREVCCHLA 151
QY 146 ATSMILASLIAGHTMYTMHLPCVSWIEIRHLCEIPPLIKACADTSRYELIYVTGT 205
DB 152 IVSMGMCIVGLQGTNIXISLNFQPCIEIDHFCDELPLALACGDTSQNEAIFVAIL 211
QY 206 FULLPISAIYASTVIVFTYLRMPSNKGKALVTCSSHLIVGMFGATFMYVLPSSF 265
DB 212 CISSPFLVILYSYRILVAVLWMSPEGRKHALSTCSSHLVLTFLYGSVFTYLRKSS 271
QY 266 HSPKODNISVFYITVPALNPLIYSLRNKVMKALRVL 305
DB 272 HSPGMDKLALFYAVTSMINFIYSLRNKVMKALRVL 311

RESULT 12
US-08-988-876-7
Sequence 7, Application US/08988876
Patent No. 6063596
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
TITLE OF INVENTION: WITH IMMUNE RESPONSE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PasteSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,876
FILING DATE: Herewith
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ballings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0441 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 314 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 32086
US-08-988-876-7

Query Match 39.5%; Score 632; DB 3; Length 314;
Best Local Similarity 41.4%; Pred. No. 3.4e-50;
Matches 125; Conservative 57; Mismatches 120; Indels 0; Gaps 0;

QY 4 RNTLSGFLVIGLINDSGSPFLYATFTILYMLALTSNGLLITFARLHMPYLL 63
DB 4 QNCTSIDFLLELPQEQONCYALFLAMYLTLLGNLLITVLRLDHLHMPYLL 63
QY 64 GOLSLMDLFTSVVTPKALADFLRENTISFGGALOMFLATMGSABDLLEAFAYDRY 123
DB 64 SNISFBDLCRSSYTIKRLQNMQNDPSIPYACDLQMYFLLFGDESLFLVAMADRY 123
QY 124 VAIChPLKYMTMSPRVCWIMVATSWILASLIAGHTMYTMHLPCVSWIEIRHLCEIP 163
DB 124 VAICPLHYTAIMSPLCLALVALSWLTFHMLHTLMARLCFCADNVIPIHFCMGA 183
QY 184 LKTLACADTSRYELIYVTGFTLLPISAVSYTLVFTYLRMPSNKGKALVTCSS 243
DB 184 LKTLASDTRVNMVAVIFIMGLILVIFLLILGSYARIVSILKVPSSKGLCAFTCS 243
QY 244 HLIVGMFGATFMYVLPSSFHSPKODNISVFYITVPALNPLIYSLRNKVMKALRV 303
DB 244 HLSVSLFTYGVIGLYCSSANSSTLKDVTWAMMYVTVTMLNDFIYSLRNKVMKALRV 303
QY 304 VL 305
DB 304 VI 305

RESULT 13
US-09-546-986A-8
Sequence 8, Application US/09546986A
Patent No. 6635741
GENERAL INFORMATION:
APPLICANT: Powers, Scott
APPLICANT: Yang, Jianxin
APPLICANT: Cutler, Gene
APPLICANT: Tularik, Inc.
TITLE OF INVENTION: No. 6635741e1 G-Protein Coupled Receptors
FILE REFERENCE: 018781-004720US
CURRENT APPLICATION NUMBER: US/09/546,986A
CURRENT FILING DATE: 2002-04-30
PRIORITY APPLICATION NUMBER: US 09/524,730

```

; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-546-986A-8

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Query Match	38.5%;	Score 616;	DB 4;	Length 334;
Best Local Similarity	40.6%;	Pred. NO. 1.1e-48;		
Matches 121; Conservative	59;	Mismatches 118;	Indels 0;	Gaps 0;

QY 10 SGIIVGLINDSSPELLVATFIILIMALTNSGLLAIITAEALHPWVLLIGOLSIM 69
 Db 30 AGFIIIGFSDYAOQKVFLVILILITVLITLIGNTIIILVSRLEPGLNPMVIFELSHSEFL 89
 QY 70 DLIFTSVYTPKALADFLRRENTISFEGCALQMFALITNGSADLLILAFMAAYDYVAICHP 123
 Db 90 YRCFTSSVYFOLLVNLMEPMKTIAYGGCLVHLYNSHALGSTCEVLPALMSCDRYAVACRP 144
 QY 130 LKNTLMSPRVCWIMVATSMILASLIAGHTWYTHLPFCVSWELRHLCIEPIPLTKAC 185
 Db 150 LHTTVLMHILCHALASMAISGIATLVQSLITLQLPFCGRQVDHITGCVPLIKIAC 203
 QY 190 ADTSRYELIITYGTVFLILPISAIIVASYTVLVFLTEMPNSBEKKALVTCSSHLIVYG 245
 Db 210 VGTTFNEABELVASIIFLIVPVSFLIVSGYIAHAVLIRIKATGQRKAFCTCFPHLIVTV 265
 QY 250 MFYCATFMVVLPSFSFKODNIISVFETIYTPALNPLIYSLRNKXEMRLARSLVLR 307
 Db 270 IFYGTITIFMYLPAKRSRDQGFVSLFIVTVTRMLNPLIITLRIKEXGKMLKRVLAK 327

RESULT 14
US-09-524-730-8
; Sequence 8, Application US/09524730

Query Match	38.5%;	Score 616;	DB 4;	Length 334;
Best Local Similarity	40.6%;	Pred. No. 1.1e-48;		
Matches 121;	Conservative 59;	Mismatches 118;	Indels 0;	Gaps 0

[illegible]

D_b 210 VGTTEENAELEFVASLILFLIVPSVFLTSSGVIATAHVLRIKSGATGRQAKPCTCSHLTVVT 269
O_y 250 MEYGATFMYYLPSSFHSFKPDNIISVFYITVPALNPLIYSIRNKWEVRALRVYLCK 307
D_b 270 IFYGIIMFYIQPAKSRSRQDKFSLFTYVTVTRMLNPILITYLRIRSEVGALKKVLA 327

RESULT 15
US-09-546-986A-2
; Sequence 2, Application US/09546986A

Query Match	37.8%	Score 605;	DB 4;	Length 310;
Best Local Similarity	40.8%	Pred. No. 1e-47;		
Matches 122;	Conservative 63;	Mismatches 108;	Indels 6;	Gaps 2

[illegible]

Search completed: August 18, 2004, 08:59:34
Job time : 20 secs

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OM protein - protein search, using sw model

Run on: August 18, 2004, 08:58:44 ; Search time 46 Seconds

(Without alignments)
2156.543 Million cell updates/sec

Title: US-10-024-444B-2

Perfect score: 1602
Sequence: 1 MELNSTLGSFGLVGIIND.....VNRALRVIGKYLIAHSTL 316

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1292805 seqs, 313927144 residues

Total number of hits satisfying chosen parameters: 1292805

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1602	100.0	316	14	US-10-024-444B-2
2	1393	87.0	324	10	US-09-974-591-12
3	1393	87.0	324	10	US-09-974-591-14
4	1393	87.0	324	10	US-09-777-789-11
5	1393	87.0	324	10	US-09-974-149-12
6	1393	87.0	324	10	US-09-974-149-14
7	1390	86.8	316	9	US-09-886-055-197
8	1390	86.8	316	10	US-09-777-789-9
9	1390	86.8	316	10	US-09-804-291-197
10	1390	86.8	316	11	US-09-912-976-53
11	1390	86.8	316	11	US-09-965-422-58
12	1390	86.8	316	12	US-10-343-650A-514
13	1390	86.8	316	14	US-10-220-382-18
14	1390	86.8	316	14	US-10-017-161-310
15	1390	86.8	316	14	US-10-024-444B-3

16	1390	86.8	316	15	US-10-300-846-26	Sequence 26, Appl
17	1390	86.8	316	15	US-10-292-798-276	Sequence 276, App
18	1390	86.8	316	10	US-09-795-271-51	Sequence 51, Appl
19	1324	82.6	316	14	US-10-024-444B-4	Sequence 4, Appl
20	1312	81.9	316	11	US-09-912-976-51	Sequence 51, Appl
21	1312	81.9	316	14	US-10-024-444B-5	Sequence 5, Appl
22	1308	81.6	316	11	US-09-912-976-50	Sequence 50, Appl
23	1308	81.6	316	11	US-09-965-422-60	Sequence 60, Appl
24	1308	81.6	316	14	US-10-024-444B-6	Sequence 6, Appl
25	1304	81.4	316	10	US-09-777-789-41	Sequence 41, Appl
26	1304	81.4	316	10	US-09-777-789-42	Sequence 42, Appl
27	1304	81.4	316	10	US-09-777-789-46	Sequence 46, Appl
28	1304	81.4	316	10	US-09-777-789-47	Sequence 47, Appl
29	1304	81.4	316	10	US-09-795-271-48	Sequence 48, Appl
30	1304	81.4	316	11	US-09-912-976-52	Sequence 52, Appl
31	1304	81.4	316	11	US-09-965-422-56	Sequence 56, Appl
32	1304	81.4	316	14	US-10-024-444B-7	Sequence 7, Appl
33	1304	81.4	316	15	US-10-005-041A-104	Sequence 104, Appl
34	1248	77.9	319	10	US-09-795-271-50	Sequence 50, Appl
35	1248	77.9	319	11	US-09-965-422-57	Sequence 57, Appl
36	1203	75.1	315	10	US-09-795-271-49	Sequence 49, Appl
37	1203	75.1	315	11	US-09-965-422-59	Sequence 59, Appl
38	1203	75.1	315	11	US-09-981-566A-71	Sequence 71, Appl
39	1203	75.1	315	15	US-10-005-041A-105	Sequence 105, App
40	1083	67.6	210	14	US-10-017-161-636	Sequence 636, App
41	839	52.4	317	11	US-09-965-422-16	Sequence 16, Appl
42	833	52.0	317	9	US-09-886-055-479	Sequence 479, App
43	833	52.0	317	10	US-09-964-291-479	Sequence 14, Appl
44	833	52.0	317	11	US-09-805-422-14	Sequence 2, Appl
45	833	52.0	317	14	US-10-017-161-2	

ALIGNMENTS

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RESULT 1
US-10-024-444B-2
; Sequence 2, Application US/10024444B
; Publication No. US20030165858A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Smithson, Glenda
; APPLICANT: Stone, David
; APPLICANT: Bin-Yang, Ruey
; APPLICANT: Conley, Pamela B.
; APPLICANT: Hart, Matthew
; APPLICANT: Tomlinson, James E.
; APPLICANT: Topper, James N.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Casman, Stacie J.
; APPLICANT: MacDougall, John R.
; APPLICANT: Shlomiv, Edinger R.
; TITLE OF INVENTION: No. US20030165858A1 GPCR-Like Proteins and Nucleic Acids Encodi
; FILE REFERENCE: 21402-224 AG
; CURRENT APPLICATION NUMBER: US/10/024,444B
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/256635
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 316
; TYPE: PPT
; ORGANISM: Human
US-10-024-444B-2
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Query Match 100.0%; Score 1602; DB 14; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.5e-144;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELNSTLGSFGLVGIINDSGSPDLLVATFTIYMLATLTSNGILLATITTEARLHPMY 60

Db 1 MELRNSTLSSGFLVGLINDSGSPDLLATFTLLMLALTSNGLLLATTEARLHPMY 60
QY 61 LLLGQLSMDLFTSVTPKALADFLRRENTISFGGALOMFLATMGSEDLILAFMAY 120
Db 61 LLLGQLSMDLFTSVTPKALADFLRRENTISFGGALOMFLATMGSEDLILAFMAY 120
QY 121 DRVVAICHPLKWTMTSPRCWIMVATSWILASILAIGHMTYMHLPFCVSWETRHLCE 180
Db 121 DRVVAICHPLKWTMTSPRCWIMVATSWILASILAIGHMTYMHLPFCVSWETRHLCE 180
QY 181 IPELKLACADTSRYELIIVYGVTFLLPISAIVASYTLVLFVLRMPSEGRKKALVT 240
Db 181 IPELKLACADTSRYELIIVYGVTFLLPISAIVASYTLVLFVLRMPSEGRKKALVT 240
QY 241 CSSHLIVGMFYGAATFMYVLPSSFSHPKODNIISVFTYITVPALNPLIYSLRNKEVMA 300
Db 241 CSSHLIVGMFYGAATFMYVLPSSFSHPKODNIISVFTYITVPALNPLIYSLRNKEVMA 300
QY 301 LRRVLGKYLILAHSTL 316
Db 301 LRRVLGKYLILAHSTL 316

RESULT 2

US-09-974-591-12

Sequence 12, Application US/09974591

Publication No. US20030059830A1

GENERAL INFORMATION:

APPLICANT: Alsobrook II, John P

APPLICANT: Burgess, Catherine E

APPLICANT: Grose, William M

APPLICANT: Lepley, Denise M

APPLICANT: Padigaru, Murajidhara

APPLICANT: Spytek, Kimberly A

TITLE OF INVENTION: No. US20030059830A1 Single Nucleotide Polymorphisms for Olfaction

TITLE OF INVENTION: Receptor-like Polypeptides and Nucleic Acids Encoding

TITLE OF INVENTION: the Same

FILE REFERENCE: 15966-654 CIP

CURRENT APPLICATION NUMBER: US/09/974, 591

CURRENT FILING DATE: 2001-10-09

PRIOR APPLICATION NUMBER: 60/245,292

PRIOR FILING DATE: 2000-11-02

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 12

LENGTH: 324

TYPE: PRT

ORGANISM: Homo sapiens

US-09-974-591-12

Query Match 87.0%; Score 1393; DB 10; Length 324;

Best Local Similarity 87.3%; Pred. No. 1.4e-124;

Matches 276; Conservative 16; Mismatches 24; Indels 0; Gaps 0;

QY 1 MELRNSTLSSGFLVGLINDSGSPDLLATFTLLMLALTSNGLLLATTEARLHPMY 60
Db 1 MELRNSTLSSGFLVGLINDSGSPDLLATFTLLMLALTSNGLLLATTEARLHPMY 60
QY 9 MELNFTLSSGFLVGLINDSGSPDLLATFTLLMLALTSNGLLLATTEARLHPMY 68
Db 9 MELNFTLSSGFLVGLINDSGSPDLLATFTLLMLALTSNGLLLATTEARLHPMY 68
QY 61 LLLGQLSMDLFTSVTPKALADFLRRENTISFGGALOMFLATMGSEDLILAFMAY 120
Db 61 LLLGQLSMDLFTSVTPKALADFLRRENTISFGGALOMFLATMGSEDLILAFMAY 120
QY 69 LLLGQLSMDLFTSVTPKALADFLRRENTISFGGALOMFLATMGSEDLILAFMAY 128
Db 69 LLLGQLSMDLFTSVTPKALADFLRRENTISFGGALOMFLATMGSEDLILAFMAY 128
QY 121 DRVVAICHPLKWTMTSPRCWIMVATSWILASILAIGHMTYMHLPFCVSWETRHLCE 180
Db 121 DRVVAICHPLKWTMTSPRCWIMVATSWILASILAIGHMTYMHLPFCVSWETRHLCE 180
QY 181 IPELKLACADTSRYELIIVYGVTFLLPISAIVASYTLVLFVLRMPSEGRKKALVT 240
Db 181 IPELKLACADTSRYELIIVYGVTFLLPISAIVASYTLVLFVLRMPSEGRKKALVT 240
QY 241 CSSHLIVGMFYGAATFMYVLPSSFSHPKODNIISVFTYITVPALNPLIYSLRNKEVMA 300
Db 241 CSSHLIVGMFYGAATFMYVLPSSFSHPKODNIISVFTYITVPALNPLIYSLRNKEVMA 300

Db 249 CSSHLIVGMFYGAATFMYVLPSSFSHPKODNIISVFTYITVPALNPLIYSLRNKEVMA 308
QY 301 LRRVLGKYLILAHSTL 316
Db 309 LRRVLGKYLILAHSTL 324

RESULT 3

US-09-974-591-14

Sequence 14, Application US/09974591

Publication No. US20030059830A1

GENERAL INFORMATION:

APPLICANT: Alsobrook II, John P

APPLICANT: Burgess, Catherine E

APPLICANT: Grose, William M

APPLICANT: Lepley, Denise M

APPLICANT: Padigaru, Murajidhara

APPLICANT: Spytek, Kimberly A

TITLE OF INVENTION: No. US20030059830A1 Single Nucleotide Polymorphisms for Olfaction

TITLE OF INVENTION: Receptor-like Polypeptides and Nucleic Acids Encoding

TITLE OF INVENTION: the Same

FILE REFERENCE: 15966-654 CIP

CURRENT APPLICATION NUMBER: US/09/974, 591

CURRENT FILING DATE: 2001-10-09

PRIOR APPLICATION NUMBER: 60/245,292

PRIOR FILING DATE: 2000-11-02

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 14

LENGTH: 324

TYPE: PRT

ORGANISM: Homo sapiens

US-09-974-591-14

Query Match 87.0%; Score 1393; DB 10; Length 324;

Best Local Similarity 87.3%; Pred. No. 1.4e-124;

Matches 276; Conservative 16; Mismatches 24; Indels 0; Gaps 0;

QY 1 MELRNSTLSSGFLVGLINDSGSPDLLATFTLLMLALTSNGLLLATTEARLHPMY 60
Db 1 MELNFTLSSGFLVGLINDSGSPDLLATFTLLMLALTSNGLLLATTEARLHPMY 68
QY 9 MELNFTLSSGFLVGLINDSGSPDLLATFTLLMLALTSNGLLLATTEARLHPMY 68
Db 9 MELNFTLSSGFLVGLINDSGSPDLLATFTLLMLALTSNGLLLATTEARLHPMY 68
QY 61 LLLGQLSMDLFTSVTPKALADFLRRENTISFGGALOMFLATMGSEDLILAFMAY 120
Db 61 LLLGQLSMDLFTSVTPKALADFLRRENTISFGGALOMFLATMGSEDLILAFMAY 120
QY 69 LLLGQLSMDLFTSVTPKALADFLRRENTISFGGALOMFLATMGSEDLILAFMAY 128
Db 69 LLLGQLSMDLFTSVTPKALADFLRRENTISFGGALOMFLATMGSEDLILAFMAY 128
QY 121 DRVVAICHPLKWTMTSPRCWIMVATSWILASILAIGHMTYMHLPFCVSWETRHLCE 180
Db 121 DRVVAICHPLKWTMTSPRCWIMVATSWILASILAIGHMTYMHLPFCVSWETRHLCE 180
QY 181 IPELKLACADTSRYELIIVYGVTFLLPISAIVASYTLVLFVLRMPSEGRKKALVT 240
Db 181 IPELKLACADTSRYELIIVYGVTFLLPISAIVASYTLVLFVLRMPSEGRKKALVT 240
QY 241 CSSHLIVGMFYGAATFMYVLPSSFSHPKODNIISVFTYITVPALNPLIYSLRNKEVMA 300
Db 249 CSSHLIVGMFYGAATFMYVLPSSFSHPKODNIISVFTYITVPALNPLIYSLRNKEVMA 308
QY 301 LRRVLGKYLILAHSTL 316
Db 309 LRRVLGKYLILAHSTL 324

RESULT 4

US-09-777-789-11

Sequence 11, Application US/09777789

Publication No. US20030087815A1

GENERAL INFORMATION:

APPLICANT: Padigaru et al.

TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME

FILE REFERENCE: 15966-654

CURRENT APPLICATION NUMBER: US/09/777,789

CURRENT FILING DATE: 2001-05-11

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/ PRIOR APPLICATION NUMBER: 60/180,646
/ PRIOR FILING DATE: 2000-02-07
/ NUMBER OF SEQ ID NOS: 101
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO 11
/ LENGTH: 324
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-777-789-11

Query Match
Best Local Similarity 87.0%; Score 1393; DB 10; Length 324;
Matches 276; Conservative 16; Mismatches 24; Indels 0; Gaps 0;

QY 1 MELNSTGSGFLVGIINDSGSPPELLVATFTILVMLALTSNGLLLAITTEARLHMPY 60
DB 9 MELNMTLGSGLFVGIINDSGSPPELLCATITTLVLAISNGLLLAITTEARLHMPY 68
QY 61 LLLGQLSLMDLLFTSVTPKALADFLRRENTISFGGCAQMPALTMGSAEDLLAFMAY 120
DB 69 LLLGQLSLMDLLFTSVTPKALADFLRRENTISFGGCAQMPALTMGSAEDLLAFMAY 128
QY 121 DRYVAICHPDKMTLMSPRVCWIMVATSWILASLAIIGHMTYTMHLPCVSEIRHLCE 180
DB 129 DRYVAICHPDKMTLMSPRVCWIMVATSWILASLAIIGHMTYTMHLPCVSEIRHLCE 188
QY 181 IPEPLKACADTSRELYLIIYTGVTFLIPISAIYASVTLVFTVLRMPSNEGKKAALVT 240
DB 189 IPHLKACADTSRELYLIIYTGVTFLIPISAIYASVTLVFTVLRMPSNEGKKAALVT 248
QY 241 CSSHLIVGMFYGAATFMYLPSFSFSPKODNISVFYITVTPALNPLIYSLRKEWMA 300
DB 249 CSSHLIVGMFYGAATFMYLPSFSFSPKODNISVFYITVTPALNPLIYSLRKEWMA 308
QY 301 LRRVLGKYTLIAHSTL 316
DB 309 LRRVLGKYTLIAHSTL 324

RESULT 5
US-09-974-149-12
/ Sequence 12, Application US/09974149
/ Publication No. US20030175705A1
/ GENERAL INFORMATION:
/ APPLICANT: Alsobrook II, John P
/ APPLICANT: Burgess, Catherine E
/ APPLICANT: Grose, William M
/ APPLICANT: Lepley, Denise M
/ APPLICANT: Padigar, Muralidhara
/ APPLICANT: Spytek, Kimberly A
/ APPLICANT: Bader, Joel S
/ APPLICANT: Banas, Aruna
/ TITLE OF INVENTION: Methods of Use for No. US20030175705A1 Single Nucleotide
/ TITLE OF INVENTION: Polymorphisms of Olfactory Receptor-like Polypeptides
/ FILE REFERENCE: 15966-654UB
/ CURRENT APPLICATION NUMBER: US/09/974,149
/ PRIOR FILING DATE: 2002-05-20
/ PRIOR APPLICATION NUMBER: 60/323,755
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 12
/ LENGTH: 324
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-974-149-12

Query Match
Best Local Similarity 87.0%; Score 1393; DB 10; Length 324;
Matches 276; Conservative 16; Mismatches 24; Indels 0; Gaps 0;

QY 1 MELNSTGSGFLVGIINDSGSPPELLVATFTILVMLALTSNGLLLAITTEARLHMPY 60
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DB 9 MELNMTLGSGLFVGIINDSGSPPELLCATITTLVLAISNGLLLAITTEARLHMPY 68
QY 61 LLLGQLSLMDLLFTSVTPKALADFLRRENTISFGGCAQMPALTMGSAEDLLAFMAY 120
DB 69 LLLGQLSLMDLLFTSVTPKALADFLRRENTISFGGCAQMPALTMGSAEDLLAFMAY 128
QY 121 DRYVAICHPDKMTLMSPRVCWIMVATSWILASLAIIGHMTYTMHLPCVSEIRHLCE 180
DB 129 DRYVAICHPDKMTLMSPRVCWIMVATSWILASLAIIGHMTYTMHLPCVSEIRHLCE 188
QY 181 IPEPLKACADTSRELYLIIYTGVTFLIPISAIYASVTLVFTVLRMPSNEGKKAALVT 240
DB 189 IPHLKACADTSRELYLIIYTGVTFLIPISAIYASVTLVFTVLRMPSNEGKKAALVT 248
QY 241 CSSHLIVGMFYGAATFMYLPSFSFSPKODNISVFYITVTPALNPLIYSLRKEWMA 300
DB 249 CSSHLIVGMFYGAATFMYLPSFSFSPKODNISVFYITVTPALNPLIYSLRKEWMA 308
QY 301 LRRVLGKYTLIAHSTL 316
DB 309 LRRVLGKYTLIAHSTL 324

RESULT 6
US-09-974-149-14
/ Sequence 14, Application US/09974149
/ Publication No. US20030175705A1
/ GENERAL INFORMATION:
/ APPLICANT: Alsobrook II, John P
/ APPLICANT: Burgess, Catherine E
/ APPLICANT: Grose, William M
/ APPLICANT: Lepley, Denise M
/ APPLICANT: Padigar, Muralidhara
/ APPLICANT: Spytek, Kimberly A
/ APPLICANT: Bader, Joel S
/ APPLICANT: Banas, Aruna
/ TITLE OF INVENTION: Methods of Use for No. US20030175705A1 Single Nucleotide
/ TITLE OF INVENTION: Polymorphisms of Olfactory Receptor-like Polypeptides
/ FILE REFERENCE: 15966-654UB
/ CURRENT APPLICATION NUMBER: US/09/974,149
/ PRIOR FILING DATE: 2002-05-20
/ PRIOR APPLICATION NUMBER: 60/323,755
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 14
/ LENGTH: 324
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-974-149-14

Query Match
Best Local Similarity 87.0%; Score 1393; DB 10; Length 324;
Matches 276; Conservative 16; Mismatches 24; Indels 0; Gaps 0;

QY 1 MELNSTGSGFLVGIINDSGSPPELLVATFTILVMLALTSNGLLLAITTEARLHMPY 60
DB 9 MELNMTLGSGLFVGIINDSGSPPELLCATITTLVLAISNGLLLAITTEARLHMPY 68
QY 61 LLLGQLSLMDLLFTSVTPKALADFLRRENTISFGGCAQMPALTMGSAEDLLAFMAY 120
DB 69 LLLGQLSLMDLLFTSVTPKALADFLRRENTISFGGCAQMPALTMGSAEDLLAFMAY 128
QY 121 DRYVAICHPDKMTLMSPRVCWIMVATSWILASLAIIGHMTYTMHLPCVSEIRHLCE 180
DB 129 DRYVAICHPDKMTLMSPRVCWIMVATSWILASLAIIGHMTYTMHLPCVSEIRHLCE 188
QY 181 IPEPLKACADTSRELYLIIYTGVTFLIPISAIYASVTLVFTVLRMPSNEGKKAALVT 240
DB 189 IPHLKACADTSRELYLIIYTGVTFLIPISAIYASVTLVFTVLRMPSNEGKKAALVT 248
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Oy      241 C$SHLTVGAFMGATPMVLPSSPHSKRONIISVFITVTPALNPLIYSLNKEVMEA 300
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Db      249 C$SHLTVGAFMGATPMVLPSSPHSTRQNIISVFITVTPALNPLIISLNKEVMEA 308
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Oy      301 LRRVLGKTYILLAHSTL 316
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      309 LRRVLGKTYMLPAHSTL 324
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RESULT 7
US-09-886-055-197
; Sequence 197, Application US/09886055
; Patent No. US20020132273A1
; GENERAL INFORMATION:
; APPLICANT: STRYER, LUBERT
; APPLICANT: ZOZULYA, SERGEY
; TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
; TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS
; FILE REFERENCE: 078003-0277150
; CURRENT APPLICATION NUMBER: US/09/886,055
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,812
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 522
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 197
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-886-055-197

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Query Match	86.8%	Score 1390	DB 9	length 316
Best Local Similarity	87.0%	Pred. No. 2.6e-124		
Matches 275	Conservative 17	Mismatches 24	Indels 0	Gaps 0

Qy	1	MEJNRNPIGSGFLLVGLINDSGPELLVATFFILMLALITSGLLILALITTEALINPMY	60
Db	1	MELMNFLLSGFLLVGLINDSGPELLCATITFLVLALISGGLLLALITWEALINPMY	60
Qy	61	LLIGQSLNDLLETSTVYTPKALADPIRRRNTTISFGGCLQMFALITMGSADLLAMAY	120
Db	61	LLIGQSLNDLLETSTVYTPKALADPIRRRNTTISFGGCLQMFALITMGSADLLAMAY	120
Qy	121	DRYVAICHPLEKWTMLSPVCWIMVATSWILASLIAIGHTMYMLPVCVSWEIRHLCE	180
Db	121	DRYVAICHPLEKWTMLSSRACWIMVATSWILASLIAITYVTMHPCCRAQEIFRLICE	180
Qy	181	IPPLIKACADTSTRYEILITYTGVTFLPLPISAIYASVLYLFTYLRMPSNEGRKALVT	240
Db	181	IPPLIKACADTSTRYEIMYVMKVYPLIPSLAIIASTYQILITLVLMHPSNEGRKALVT	240
Qy	241	CSHSLIYVGNFYGAATFMVLPSSFSHPXQDNIISVFYITVTPALNPLIYSIRNKEVWRA	300
Db	241	CSHSLIYVGNFYGAATFMVLPSSFSHSTRQDNIISVFYITVTPALNPLIYSIRNKEVWRA	300
Qy	301	LRRTYIKYITLLAHSSTL 316	
Db	301	LRRTYIKYITLLAHSSTL 316	

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RESULT 8
US-09-777-789-9
; Sequence 9, Application US/09777789
; Publication No. US20030087815A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru et al.
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15566-654
; CURRENT APPLICATION NUMBER: US/09/777,789
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/180,646
; PRIOR FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 101

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-777-789-9

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Query Match	86.8%;	Score 1390;	DB 10;	Length 316;
Best Local Similarity	87.0%;	Pred. No. 2.6e-124;		
Matches 275;	Conservative 17;	Mismatches 24;	Indels 0;	Gaps 0;

QY	1	MELNKSTIGSGPFIIVGINDSGSPBLXATFIIFMLATSGULLALITLARLAMP	60
Db	1	MELNFTIGSGPFIIVGINDSGSPBLTATITIIIVLALISNGULLIATTEARLAMPAY	60
QY		ILLIOLSLMDLFTSVVTPKALADELRENTISFGCALQWFLATLTMGSAEDLLAFMAY	120
Db	61	ILLQOLSLMDLFTSVVTPKALADELRENTISFGCALQWFLATLTMGSAEDLLAFMAY	120
QY	121	DRYYAICHPLKMYTMLSPPVCMIVATSMIILASLIAIGHTMYTMBLPCVSWIEIRHLCE	180
Db	121	DRYYAICHPLTYMTLMSRACIMVATSMIILASLIAITYVTMHPFRAOIEIRHLCE	180
QY	161	IPPLIKLACAPTSRELIIVYTVGFELLPIISAIYASYTLMFTVLRPMSNEGRKALVT	240
Db	161	IPHLIKACAPTSRELMVYTMGVTFLLPISLAIILASTYQIILLTYLHMSNEGRKALVT	240
QY	241	CSHLLIVGMFYGAATEMYVLPSSFSHPKODNIIISVFTIIVTPALNPLIYSLRNKEVMA	300
Db	241	CSHLLIVGMFYGAATEMYVLPSSFSHSTRODNIIISVFTIIVTPALNPLIYSLRNKEVMA	300
QY	301	LRRVYGRYIILAHSTL 316	
Db	301	LRRVYGRYIILAHSTL 316	

RESULT 9
US-09-804-291-197
; Sequence 197, Application US/09804291
; Publication No. US20030088059A1

```

/ TITLE OF INVENTION: HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME
/ FILE REFERENCE: P 0278005
/ CURRENT APPLICATION NUMBER: US/09/804,291
/ CURRENT FILING DATE: 2001-03-13
/ PRIOR APPLICATION NUMBER: 60/188,914
/ PRIOR FILING DATE: 2000-03-13
/ PRIOR APPLICATION NUMBER: 60/192,033
/ PRIOR FILING DATE: 2000-03-24
/ PRIOR APPLICATION NUMBER: 60/198,474
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/199,335
/ PRIOR FILING DATE: 2000-04-24
/ PRIOR APPLICATION NUMBER: 60/207,702
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/213,849
/ PRIOR FILING DATE: 2000-06-23
/ PRIOR APPLICATION NUMBER: 60/226,534
/ PRIOR FILING DATE: 2000-08-16
/ PRIOR APPLICATION NUMBER: 60/230,732
/ PRIOR FILING DATE: 2000-09-07
/ PRIOR APPLICATION NUMBER: 60/266,862
/ PRIOR FILING DATE: 2001-02-07
/ NUMBER OF SEQ ID NOS: 529
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 197
/ LENGTH: 316
/ TYPE: PRT
/ ORGANISM: Homo sapiens

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Query Match	86.8%;	Score 1390;	DB 10;	Length 316;
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Best Local Similarity 87.0%; Pred. No. 2,6e-124;
Matches 275; Conservative 17; Mismatches 24; Indels 0; Gaps 0;

QY 1 MELRNSTLGGFLLVGIINDSGSPELIVYTFITLVMALTSNGLLIATTEARLHMPY 60
DB 1 MELMNTLSSGFLVGIINDSGSPELICTITITLILALISNGLLIATTEARLHMPY 60
QY 61 LILGQSLMDLFTSVTPKALADFLRRENTISFGGCAQMFALTMGAEDLLAFMAY 120
DB 61 LILGQSLMDLFTSVTPKALADFLRRENTISFGGCAQMFALTMGAEDLLAFMAY 120
QY 121 DRYVALCHPLKWTMTLSPRCVIMVATSWITLALISGHTMTMHPFCVSEIRHLCE 180
DB 121 DRYVALCHPLKWTMTLSPRCVIMVATSWITLALISGHTMTMHPFCVSEIRHLCE 180
QY 181 IPELKLACADTSRYELIYVTVFELLIPISAVSYTLVLFVTRMPSNEGRKALVT 240
DB 181 IPELKLACADTSRYELIYVTVFELLIPISAVSYTLVLFVTRMPSNEGRKALVT 240
QY 241 CSNHLVGMFGAATFMVLPSSFSHPKODNIISVFYITVPALNPLIYSLNKEVMA 300
DB 241 CSNHLVGMFGAATFMVLPSSFSHPKODNIISVFYITVPALNPLIYSLNKEVMA 300
QY 301 LRRVIGKYLILAHSTL 316
DB 301 LRRVIGKYLILAHSTL 316

RESULT 10

US-09-912-976-53
; Sequence 53, Application US/09912976
; Publication No. US20030212255A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mezes, Peter
; APPLICANT: Burgess, Catherine
; APPLICANT: Casman, Stacie
; APPLICANT: Grose, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Gerlach, Valerie L
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glenda
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-070
; CURRENT APPLICATION NUMBER: US/09/912,976
; PRIOR APPLICATION NUMBER: 60/221,336
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/238,333
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/260,675
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 60/271,025
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/278,164
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/280,876
; PRIOR FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-912-976-53

Query Match 86.8%; Score 1390; DB 11; Length 316;
Best Local Similarity 87.0%; Pred. No. 2,6e-124;
Matches 275; Conservative 17; Mismatches 24; Indels 0; Gaps 0;

QY 1 MELRNSTLGGFLLVGIINDSGSPELIVYTFITLVMALTSNGLLIATTEARLHMPY 60

DB 1 MELMNTLSSGFLVGIINDSGSPELICTITITLILALISNGLLIATTEARLHMPY 60
QY 61 LILGQSLMDLFTSVTPKALADFLRRENTISFGGCAQMFALTMGAEDLLAFMAY 120
DB 61 LILGQSLMDLFTSVTPKALADFLRRENTISFGGCAQMFALTMGAEDLLAFMAY 120
QY 121 DRYVALCHPLKWTMTLSPRCVIMVATSWITLALISGHTMTMHPFCVSEIRHLCE 180
DB 121 DRYVALCHPLKWTMTLSPRCVIMVATSWITLALISGHTMTMHPFCVSEIRHLCE 180
QY 181 IPELKLACADTSRYELIYVTVFELLIPISAVSYTLVLFVTRMPSNEGRKALVT 240
DB 181 IPELKLACADTSRYELIYVTVFELLIPISAVSYTLVLFVTRMPSNEGRKALVT 240
QY 241 CSNHLVGMFGAATFMVLPSSFSHPKODNIISVFYITVPALNPLIYSLNKEVMA 300
DB 241 CSNHLVGMFGAATFMVLPSSFSHPKODNIISVFYITVPALNPLIYSLNKEVMA 300
QY 301 LRRVIGKYLILAHSTL 316
DB 301 LRRVIGKYLILAHSTL 316

RESULT 11

US-09-965-422-58
; Sequence 58, Application US/09965422
; Publication No. US20030216545A1
; GENERAL INFORMATION:
; APPLICANT: Spylek, Kimberly A
; APPLICANT: Casman, Stacie
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Dickson, Kevin
; APPLICANT: Vernet, Corine
; APPLICANT: Spaderna, Steven K
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: Edinger, Shlomit
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glenda
; APPLICANT: Li, Li
; APPLICANT: Malpankar, Uriel M
; APPLICANT: Taylor, Sarah
; APPLICANT: Gunther, Erik
; APPLICANT: Tchernyev, Veliar T
; TITLE OF INVENTION: No. US0030216545A1 Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21401-132
; CURRENT APPLICATION NUMBER: US/09/965,422
; PRIOR APPLICATION NUMBER: 60/237,581
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/236,286
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/236,284
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/237,581
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/238,735
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/240,736
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/260,019
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,338
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/262,156
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/262,498
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/263,133
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,691
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/266,109

PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/271,634
PRIOR FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 127
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 58
LENGTH: 316
TYPE: PRT
ORGANISM: Homo sapiens
US-09-965-422-58

Query Match 86.8%; Score 1390; DB 11; Length 316;
Best Local Similarity 87.0%; Pred. No. 2,6e-124;
Matches 275; Conservative 17; Mismatches 24; Indels 0; Gaps 0;

QY 1 MELNSTLGSGLIIVGILNDSGPELLYATFTIYMLATLNSGLLLAITEARLHPMY 60
DB 1 MELNFTLGSGLIIVGILNDSGPELLCATITTIYLLALISNGLLAITEARLHPMY 60
QY 61 LLLGQLSIMDLFTSVTPKALADFLRENTISFGCALQMFALTWGABDILLAFMAY 120
DB 61 LLLGQLSIMDLFTSVTPKALADFLRENTISFGCALQMFALTWGABDILLAFMAY 120
QY 121 DRYVAICHPKMTLMSRVCWIMVATSWILASILAIGHMTYMLPFCVSWETRHLICE 180
DB 121 DRYVAICHPMTLMSRACMLVATSWILASILAIYTYVMHYPCRAQETIRHLICE 180
QY 181 IPLLKLCADTSRYELIYVTGTFLLPISATVASYTLVFTVLRMPSNEGRKKALVT 240
DB 181 IPLLKLCADTSRYELIYVTGTFLLPISATVASYTLVFTVLRMPSNEGRKKALVT 240
QY 241 CSSHLIVGMFYGAATFMYVLPSSFHSPKQDNIISVFYITVPALNPLIYSLRKEVWRA 300
DB 241 CSSHLIVGMFYGAATFMYVLPSSFHSTRQDNIISVFYITVPALNPLIYSLRKEVWRA 300
QY 301 LRRVIGKYLIAHSTL 316
DB 301 LRRVIGKYLIAHSTL 316

RESULT 12
US-10-343-650A-514
Sequence 514, Application US/10343650A
Publication No. US20040067499A1
GENERAL INFORMATION:
APPLICANT: HAGA, TATSUYA
TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
FILE REFERENCE: 31671-186347
CURRENT APPLICATION NUMBER: US/10/343,650A
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: JP 2000/237818
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: JP 2001/34434
PRIOR FILING DATE: 2001-02-13
NUMBER OF SEQ ID NOS: 694
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 514
LENGTH: 316
TYPE: PRT
ORGANISM: Homo sapiens
US-10-343-650A-514

Query Match 86.8%; Score 1390; DB 12; Length 316;
Best Local Similarity 87.0%; Pred. No. 2,6e-124;
Matches 275; Conservative 17; Mismatches 24; Indels 0; Gaps 0;

QY 1 MELNSTLGSGLIIVGILNDSGPELLYATFTIYMLATLNSGLLLAITEARLHPMY 60
DB 1 MELNFTLGSGLIIVGILNDSGPELLCATITTIYLLALISNGLLAITEARLHPMY 60
QY 61 LLLGQLSIMDLFTSVTPKALADFLRENTISFGCALQMFALTWGABDILLAFMAY 120
DB 61 LLLGQLSIMDLFTSVTPKALADFLRENTISFGCALQMFALTWGABDILLAFMAY 120

QY 121 DRYVAICHPKMTLMSRVCWIMVATSWILASILAIGHMTYMLPFCVSWETRHLICE 180
DB 121 DRYVAICHPMTLMSRACMLVATSWILASILAIYTYVMHYPCRAQETIRHLICE 180
QY 181 IPLLKLCADTSRYELIYVTGTFLLPISATVASYTLVFTVLRMPSNEGRKKALVT 240
DB 181 IPLLKLCADTSRYELIYVTGTFLLPISATVASYTLVFTVLRMPSNEGRKKALVT 240
QY 241 CSSHLIVGMFYGAATFMYVLPSSFHSPKQDNIISVFYITVPALNPLIYSLRKEVWRA 300
DB 241 CSSHLIVGMFYGAATFMYVLPSSFHSTRQDNIISVFYITVPALNPLIYSLRKEVWRA 300
QY 301 LRRVIGKYLIAHSTL 316
DB 301 LRRVIGKYLIAHSTL 316

RESULT 13
US-10-220-382-18
Sequence 18, Application US/10220382
Publication No. US2003011911A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: LAL, Preeti
APPLICANT: TANG, Y. Tom
APPLICANT: PATTERSON, Chandra
APPLICANT: YAO, Monique G.
APPLICANT: SHIH, Leo L.
APPLICANT: TRIBOULEY, Catherine
APPLICANT: LU, Dzung Anna M.
APPLICANT: YUE, Henry
APPLICANT: KHAN, Farrah A.
APPLICANT: POLICKY, Jennifer L.
APPLICANT: AU-YOUNG, Janice
APPLICANT: YANG, Junming
APPLICANT: HARLAND, Lee
APPLICANT: WALSH, Roderick T.
APPLICANT: LO, Terence P.
APPLICANT: BOROMSKY, Mark L.
TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
FILE REFERENCE: PI-0044 PCT
CURRENT APPLICATION NUMBER: US/10/220,382
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,854; 60/188,384; 60/190,453; 60/190,730
PRIOR FILING DATE: 2000-03-03; 2000-03-10; 2000-03-17; 2000-03-20
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PERL Program
SEQ ID NO 18
LENGTH: 316
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: incyte ID No. US2003011911A1 7472446CD1
US-10-220-382-18

Query Match 86.8%; Score 1390; DB 14; Length 316;
Best Local Similarity 87.0%; Pred. No. 2,6e-124;
Matches 275; Conservative 17; Mismatches 24; Indels 0; Gaps 0;

QY 1 MELNSTLGSGLIIVGILNDSGPELLYATFTIYMLATLNSGLLLAITEARLHPMY 60
DB 1 MELNFTLGSGLIIVGILNDSGPELLCATITTIYLLALISNGLLAITEARLHPMY 60
QY 61 LLLGQLSIMDLFTSVTPKALADFLRENTISFGCALQMFALTWGABDILLAFMAY 120
DB 61 LLLGQLSIMDLFTSVTPKALADFLRENTISFGCALQMFALTWGABDILLAFMAY 120
QY 121 DRYVAICHPKMTLMSRVCWIMVATSWILASILAIGHMTYMLPFCVSWETRHLICE 180
DB 121 DRYVAICHPMTLMSRACMLVATSWILASILAIYTYVMHYPCRAQETIRHLICE 180

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